

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: August 19, 2003, 15:30:30 ; Search time 124 Seconds  
(Without alignments)  
2694.573 Million cell updates/sec

C	Title: US-09-494-297-2	Scoring table: BLOSUM62	Sequence: 8, Appli
C	Perfect score: 3945	Xgapop 10.0 , Xgapext 0.5	Sequence 457, APP
C	Sequence: .	Ygapop 10.0 , Ygapext 0.5	Sequence 461, APP
C	Scanned: 569978 seqs, 220691566 residues	Fgapop 6.0 , Fgapext 7.0	Sequence 465, APP
C	Total number of hits satisfying chosen parameters: 1139956	DelPop 6.0 ; Delext 7.0	Sequence 1, Appli
C	Minimum DB seq length: 0		Sequence 60, Appli
C	Maximum DB seq length: 200000000		Sequence 1, Appli
C	Post-processing: Minimum Match 0%		Sequence 2477, APP
C	Maximum Match 100%		Sequence 419, APP
C	Listing first 45 summaries		Sequence 417, APP
C	Command line parameters:		Sequence 9, Appli
C	-MOPBL=frame+ p2n .model -DEV=1P		Sequence 9, Appli
C	-Q-/cgn2_1/USPTO_spool/US09494297/runat_13082003_122947_28128/app_query.fasta_1.903		Sequence 9, Appli
C	-DB=ISSUED_PATENTS_NA -QMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0		Sequence 7, Appli
C	-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40 cdi		Sequence 6, Appli
C	-LIST=45 -DOCALIGN=2000 -THR_SOREPCT=.7HR_MAX=100 -THR_MIN=.000 -ALIGN=15		Sequence 6, Appli
C	-MODE=LOCAL -OUTFMT=PTO -NORMEXT=.HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000		Sequence 11, Appli
C	-USER=US09494297 @CGN_1_1_49_0runat_13082003_122947_28128 -NCPU=6 -ICPU=3		Sequence 1, Appli
C	-NO_MMAP -LARGEQUERY -NEC_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG		Sequence 1, Appli
C	-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAP=10 -XGAPEXT=0.5 -FGAP=6		Sequence 1, Appli
C	-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELPOP=6 -DELEXT=7		Sequence 1, Appli
C	-MOPBL=frame+ p2n .model -DEV=1P		Sequence 14, Appli
C	-Q-/cgn2_1/USPTO_spool/US09494297/runat_13082003_122947_28128/app_query.fasta_1.903		Sequence 25, Appli
C	-DB=ISSUED_PATENTS_NA -QMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0		Sequence 1, Appli
C	-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40 cdi		Sequence 898, App
C	-LIST=45 -DOCALIGN=2000 -THR_SOREPCT=.7HR_MAX=100 -THR_MIN=.000 -ALIGN=15		Sequence 3061, App
C	-MODE=LOCAL -OUTFMT=PTO -NORMEXT=.HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000		Sequence 1, Appli
C	-USER=US09494297 @CGN_1_1_49_0runat_13082003_122947_28128 -NCPU=6 -ICPU=3		Sequence 2, Appli
C	-NO_MMAP -LARGEQUERY -NEC_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG		Sequence 2, Appli
C	-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAP=10 -XGAPEXT=0.5 -FGAP=6		Sequence 2, Appli
C	-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELPOP=6 -DELEXT=7		Sequence 2, Appli
C	RESULT 1	ALIGNMENTS	
C	US-09-107-532A-864		
C	; Sequence 64, Application US/09107532A		
C	; Patent No. 6538275		
C	; GENERAL INFORMATION:		
C	APPLICANT: Lynn A Doucette-Staam and David Bush		
C	TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO		
C	NUMBER OF SEQUENCES: 7310	ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS	
C	CORRESPONDENCE ADDRESS:		
C	ADDRESSEE: GENOME THERAPEUTICS CORPORATION		
C	STREET: 100 Beaver Street		
C	CITY: Waltham		
C	STATE: Massachusetts		
C	COUNTRY: USA		
C	ZIP: 02354		
C	COMPUTER READABLE FORM:		
C	MEDIUM TYPE: CD/ROM 1509660		
C	COMPUTER: PC		
C	OPERATING SYSTEM: <Unknown>		
C	SOFTWARE: ASCII		
C	CURRENT APPLICATION DATA:		
C	APPLICATION NUMBER: US/09/107_532A		
C	FILING DATE: 30-Jun 1998		
C	PRIOR APPLICATION DATA:		
C	APPLICATION NUMBER: 60/085_598		
C	FILING DATE: 14-May 1998		
C	APPLICATION NUMBER: 60/051571		
C	FILING DATE: July 2, 1997		
C	ATTORNEY/AGENT INFORMATION:		
C	NAME: Attiellelo, Pamela Deneka		
C	REGISTRATION NUMBER: 40_489		
C	REFERENCE/DOCKET NUMBER: GTC-012		
C	TELECOMMUNICATION INFORMATION:		
C	TELEPHONE: (781)893-5507		
C	TELEFAX: (781)893-8277		
C	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES	
C	Result No. Score Query Length DB ID Description		
1	182 4.6 2187 4 US-09-107_532A-864 Sequence 864, App		
2	178 4.5 2694 2 US-08-867-911-2 Sequence 2, Appli		
3	178 4.5 2694 3 US-09-074_658-2 Sequence 2, Appli		
4	178 4.5 7650 2 US-08-867_941-1 Sequence 1, Appli		
5	178 4.5 7650 3 US-09-074_658-1 Sequence 1, Appli		
6	176 4.5 2718 3 US-09-074_658-69 Sequence 69, Appli		
7	161 4.1 4249 4 US-09-071_035_403 Sequence 403, App		
8	161 4.1 4359 4 US-09-071_035_401 Sequence 401, App		
9	152 3.9 5547 4 US-08-051_567-B-48 Sequence 48, Appli		
10	152 3.9 7551 4 US-08-851_567-B-45 Sequence 46, Appli		
11	150 3.8 3531 2 US-08-014_402-1 Sequence 1, Appli		
12	150 3.8 3698 4 US-09-327_536-1 Sequence 1, Appli		

INFORMATION FOR SEQ ID NO: 864:

SEQUENCE CHARACTERISTICS:

LENGTH: 2187 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

FEATURE:

NAME/KEY: misc\_feature

LOCATION: (B) LOCATION 1 .. 2187

SEQUENCE DESCRIPTION: SEQ ID NO: 864:

US-09-107-532A-864

Alignment Scores:

Pred. No.: 3.41e-09

Score: 182.00

Percent Similarity: 34.82%

Best Local Similarity: 20.92%

Query Match: 4.61%

DB: DB:

US-09-494-297-2 (1-757) x US-09-107-532A-864 (1-2187)

QY 72 TrpTyr-----GlyTyrGluSerTyrValArgGlyHis-ProTyrTyr 85

Db 468 TGGTACACTTCAGTCAGAAGAGTGCGGGAGAACGTCTACGCTCA---- 519

Qy 85 rLysGlnPheArgValAlaHisAspLeuArgValAsnLeuGlySer----ArgSe 103

Db 520 -----TCTATTCATAGAAATTACATCAAGAG 551

Qy 103 rTyGlnValTyrCysPheAsnLeuLysAlaPheProLeuGlySerAspSerSerVa 123

Db 552 CAAATCCATTACCAAGCAGA----ATCCAACAGAAATGAGGAGTCATCCAAA 638

Qy 123 LysLysTyrTyrLysLysHisAspGlyTleserThrLysPheGluAspTyr---- 140

Db 639 TTCTGGTATCAAATGACGCCGACAACTTCCAGCCAAACATGTACCATGAAAT 698

Qy 151 uAsnGlnLysLeuArgAlaValMetTyrAsnGlyHisProGlnAsnAlaAsnGlyIle 171

Db 699 AGCTGAA-----AlaMetSerProArgLeuThrGlyAspGlu 151

Qy 171 tGluGlyLeuGluProLeuAsnAlaLeuArgValThrGlnGluAlaValTrpTyrTyrSe 191

Db 717 ATCTGCTAAAGCTCCGGGTCAGTCACATC----AAAAGTTGGGAGAAIT 770

Qy 191 rAspAsnAlaProLeuSerAsnProAspGlu--SerPhelysArgGluSerGluSerAs 210

Db 771 TGACACAACTACTGATGTCAGATCAAGTACTTGTGAGATTCAAGGGAA---- 825

Qy 210 nLeuValSerThrSerGlnLeuSerLeuMetArgGlnAlaLeuLysGlnLeuLeuAspR 230

Db 826 -----CATGACAATGCTGCAGCTGGAAACCGATATTGCAATTAAC 878

Qy 230 oAsnLeuAlaThr-----LysMetProLySGLnWa 240

Db 879 AGCTAAAGTACACAATACCTGGGAACGGACATGACAATTCCTGCACATAG 938

Qy 240 lProAspAspPheGln----LeuSerIlePheGluSerGluAspLySPLysTyr 258

Db 939 CGGAGAAAGTTATCAAGAGATATTACATCTCAATACATACAGGTCAGCAT 998

Qy 258 rAlysLysLysGlnAsnLeuLeuSerGlyGlyLeuValProThrLysProProThr 278

Db 999 CAGT-----TACCAACACTC-----AAAGAAATTACCTGTAC 1031

Qy 278 oGly-----AspProMetProProAsnGlnProGlnThrThrSe 292

Db 1032 AGATACGATTCTCACAAATAGATGCAATGACGTGGAAATACTAACAC 1091

Qy 292 rVal-----LeuIleArgLysTyrAlaLeuGlyAspTyrSerLysLeuIleGluG 309

Db 1092 GTTAACATGAAATTAACGAAAAATTCCCTACAGTGAA----AAGATCTATGG 1145

Qy 309 YAlaThrLeuGlnLeuThrGlyAspAsnValAsnSerPheGlnAla--ArgValPhSe 328

Db 1146 CGCTTGTTCAAATTACAGGAGATCTATGATCTACTAACAGATCATGGCACGG 1205

Qy 328 rSerAsnAspIleGlyGluArgIleGluIle---SerAspGlyLysThrThrLeuThrG 347

Db 1206 AACCTATTCTCTCCAGAAATGCAATTGCAAAAGAAATGCACTATCGTGACAGA 1265

Db 347 uLeuAsnSerProAlaGlyTyrSerTrieLeuGluProLeuThrPhiLeuValGluAlaG 367

Qy 377 ---GlnIleGluAsnProAsnLysGluIleValGluProTyrSerValGluAlaTyrAs 395

Db 1386 GTGACTATGAAATTCCCTTGTGAGTT----CCTGAGCAGTACGTAAGTATGC 1439

Qy 395 nAspPheGluGluPheSerValLeuThrHrgInAsnTyrAlaLysPheTyrTyrTyrAla 415

Db 1440 GATGCAAGGGACGGCAAGAGATAATCTATAGAGGAGCATTTCCTACAGAAAAA 1499

Qy 415 sAsnLysAsnGlySerSerGlnValValTyrCysPheAsnAlaPheLeuLysSerProP 435

Db 1500 AGAACAAATGGTACTTACAG-----CCAT 1526

Qy 435 OASPSerGlu-----AspGlyGlyLysTyrMetThrProAspPheThrThrGlyG 452

Db 1527 TGAAGCCAACACGAAATGAAAGGCTTGGCAGTTGATTCACACGCTGGAA 1586

Qy 452 uValIysTyrThrHsileAlaGlyArgAspLeuPheLysTyrThrValLysProArgS 472

Db 1587 ATATCGAGTCGTCGTAACAGCTGCTGGCTCGCGGAT-----GA 1625

Qy 472 pThrAspProAspThrPheLeuLysHistLeuLysValleGluLysGlyTyrArg 492

Db 1626 TACATGCGCCGGAAATTAGAATTCACATCGATAAT-----CCAT 1665

Qy 492 uLysGlyGlnAlaLeuGluTyrSerGlyLeuThrGluThrGlnLeuArgAlaLeuThrG 512

Db 1666 ---GGAAAATCTCATTACAGGGAAATAACCGGAGATGACCAAATAATGTTATGGAC 1718

Qy 512 nLeuAlaLeuTyrThrPheThrAspSerAlaGluLeuAspLysAspLysLeuAspTyr 532

Db 1719 GCTCACTCTCAAAATCGCTAAAGCGTTGATCTACGGTACACAAAAGGAGAC- 1776

Qy 532 rHisGlyPheGlyAspMetAsnAspSerThrLeuAlaValAlaLysIleLeuValGluY 552

Db 1777 -----AACGGACAGCATTAAGGCAAAATTCACTGCG----- 1815

Qy 552 rAlaGlnAspSerAsnProGlnLeuThrAspPhePheLeuProAsnAsn 572

Db 1816 -----GACCAGAAATG----GACTTAGA----- 1836

Qy 572 nLysTyrGlnSerLeuIleGlyThrGlnThrPheAspLeuValAspIleLea 592

Db 1837 -----TGCCTACAGAT----- 1848

Qy 592 gMetGluAspLysLysGluValIleProValThrHisAsnLeuIleArgLysThrva 612

Db 1848 ----- 1848



QY 220 ---MetArgGlnIalaLeuLysGlnLeuIleAspProAspLeuAlaThrLysMetProLys 238  
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 Db 1030 TCATTAACAGGCCAAGCTGCTTATTATGACAATCCCAACAGCAACTCCTCCAAAGC 1089  
 QY 239 GlnValProAspAspPhe-----GlnIleuserIlePheGluser 251  
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 Db 1090 TACATCAAAGCCAAATTGACACTAACAAAAAGTCATGAAACCGATGTGTTAANT 1149  
 QY 252 GluAspLys-----GlyAspLysTyrAsnLysGlyTyrGlnAsnLeuLeuAspLysGly 269  
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 Db 1150 GATGCCAAMATCACGGCACGCCACGGCTTGCTGGTAGGCCAAACTTGTGTTAATGAGAC 1209  
 QY 270 Leu-----ValProThrLysProProThrProGlyAspPro 281  
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 Db 1210 ACAGAAACGCCACCTTTATCAAAGAGCTTCACAAAGCCAAATCCCAATAACCC 1269  
 QY 282 ProMetProProAspGlnProGlnThrThrSerValLeuIleArgLysTyrAlaLeuLys 301  
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 Db 1270 -----AACCTTAAT----- 1278  
 QY 302 AspTyrSerLysLeuLeuSluGlyAlaThrLeuGlnLeuThrGlyAspAsnValAsnSer 321  
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 Db 1279 -----TCAGACACGCTAGAAGGCCGTTTAATGGTAGCTGGCAGTCAGCTG----- 1326  
 QY 322 PheGlnAlaArgValPheSerSerAsnAsp-----IleGlyGluArg 335  
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 Db 1327 -----GCCGGTAATTATTATCCAATGACAAACCCATCTATGTTCTTTGGTGTAA 1380  
 QY 335 IleGluLeuSerAspGlyThrTyThrLeuThrGluLeuAsnSerProLysGlyTyrSer 355  
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 Db 1381 CGAGACAAACAGACAACACTGRCGCCACAAAACGGTTATTTAGTCAGCTTGA 1440  
 QY 356 IleAlaGluProLeuThrPhelysValGluAlaGlyLysValTyrThrIleLeuAspGly 375  
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 Db 1441 -----AACCTGACGCGTITGCTGGTTAATGAAACGATGGCAGAAATTACAGC 1494  
 QY 376 LysGlnIleGluAsnProAsnLysGluIleValGlu-----ProTyrSerVal 391  
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 Db 1495 AAAAAGTAAATGATGCGGTGAATGAGAAAATGATAATGGTGATATCTTACAGGT 1554  
 QY 392 GluAlaTyAsnAspPhe-----GluGluLeuSerValLeuThrIle 405  
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 Db 1555 GAACCTATGATGATTCTTGGGGGAAAAAAAGCAGAATTCACCAAAGTCAC 1614  
 QY 405 Glasn-----TyrAlaLysPheTyrTyrAlaLys 415  
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 Db 1615 AGACGCACCCAASCGCTGCAGCTTATTGGCACACAGATAATTATTT 1668  
 QY 416 AsnLysAsnGlySerSerGlnValValTyrCysPheAsnAlaAspLeuLysSerPro 435  
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 Db 1669 -----ARTGCACTATATGACTATGCC 1722  
 QY 436 AspSerGluAspGlyGlyLysThrMetThrProAspPheThrThrHrglyLuVal-----  
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 Db 1723 GATGCTGTAAGCCAAACCAATTAAAGAAAAATACCTATGCCACACTAAATAG 1782  
 QY 453 ----- 453  
 Db 1783 GACACCAAGTTACCGCCATCGTGTCTACAGAAAGCCAAAGATAATAAGCCTTATACGCC 1842  
 QY 454 -----LysTyrThrHisIleLeu---GlyArgAspIlePhe----- 464  
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 Db 1843 ATTGTTGCCAAAGCTATCAGCACATCAGTTGGCGAGACGGTGTATACCGATGCCAC 1902  
 QY 465 -----LysTyrThrValAspProArgAspThrAspProAspThrPheLeu 479  
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 Db 1903 CAACCCACACACCGTATTGTCAGGCCAGATACCGACACCACCG 1962  
 QY 480 LysHistLeuLysValle----- 486  
 Db 1963 CCCAAGGCCGTTAAATTCTACAAACGCGTCTTGGCAGGCTATCTTATCCAAAAG 2022  
 QY 487 GluLysGlyTyrArgGluLysGlyGlnAlaLeuGluTyrSerGly----- 501

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RESUL 3  
 US-09-074-658-2  
 ; Sequence 2, Application US/09074658  
 ; Patent No. 6184311  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Losmore, Sheena M  
 ; APPLICANT: Run-Pan Du  
 ; APPLICANT: Quijun Wang  
 ; APPLICANT: Yang, Yan-Ping  
 ; APPLICANT: Klein, Michel H  
 ; TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA  
 ; NUMBER OF SEQUENCES: 78  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Sim & Morarney  
 ; STREET: 6th Floor, 330 University Avenue  
 ; CITY: Toronto  
 ; STATE: Ontario  
 ; COUNTRY: Canada  
 ; ZIP: M5J 1R7  
 ; COMPUTER: IBM PC compatible  
 ; MEDIUM TYPE: Floppy disk





QY 99 GluglyserArgSertryGlnValtryCysPheAsnLeuLysAlaPheProLeuGly 118  
Db 666 GAACGCCACCGT---TTTGACCCAAAGCTAACACCATTAAGCTAATGGTTAGGC 722  
QY 119 SerAspSerSerVallySlys-----TrpTrpLysLysHisAspGlyIleSerThrLys 136  
Db 723 AACTRACACACCCCTCTAAACACACTTACATCATCATCAGCAAGCTATAAG 782  
QY 137 PheGluAspTyAlaMetSerPro-----ArgLeuThr 147  
Db 783 AAAATACACAAGCCTGTGAGCCTTATGAAATATCGTTGGTAGCTGACTAAC 842  
QY 148 GluAspGluLeuAsnGlyLys-----ArgLeuThr 154  
Db 843 GAAAGCAGTCGACCCAAAAAATGCGGATCTCAAATGACAAGAACGCGATTCCAA 902  
QY 155 ---LeuArgAlaValMetTyrAsnGlyHisProGluAsnAlaAsnGlyIleMetGluGly 173  
Db 903 CCCATGCCATTTGTTTATCACGGA-----GAAACGCCAGCAGCTGCCAGT 956  
QY 174 LeuGluProLeuAsn-----ArgLeuThr 178  
Db 957 GCTGGTAATTAACTACACAGCAACTGGCTGTACCTAAGTGATGTCACAAACGCCCT 1016  
QY 179 AlaLeuArgValThrGlnGluAlaValTrpTyrSerAspAsnAlaProLeuSerAsn 198  
Db 1017 GCACTTCAGCATCAGATGAGTCAGGGGGCTATCCTAATGCCAGTGGCAATCCA 1076  
QY 199 ProAspGluSerPhelysArgGluSerGluSerAsnLeuValSerThrSerGlnLeuSer 218  
Db 1077 -----GAGGGCATGTCGTCAGTGCCCCACATTT 1109  
QY 219 Leu-----ArgLeuThr 219  
Db 1110 CTAACCGCTTCATAATAAGCACACGCCCTGCCACTTATCAGTTGGATTTGACACA 1169  
QY 220 --MetArgGlnAlaLeuLysGlnLeuLeuAspProAsnLeuAlaThrLysMetProLys 238  
Db 1110 TCATTAACAGGAAGCGCTGTCTTATTAGACATCCACACGCAACAGGCAAA 1229  
QY 239 GlnValProAspAspPhe-----GlnLeuSerIlePheGluSer 251  
Db 1230 TACATCAAAGCCAATTGACACTACCAAAAGTCTAGTGATGTCATAATT 1289  
QY 252 GluAspLeu-----GlyAspLeuValGlyGlnAsnLeuLeuSerGly 269  
Db 1290 GATGCCAAATCAACGCCAACCGCTTGCGGTACGCCAACATCTTGTGTTATGAGAAC 1349  
QY 270 Leu-----ValProThrLysProProThrProGlyAspPro 281  
Db 1350 ACAGAAACCGCACCTTTATCAAAGAGCTGTCCTAACAAAAGGCCATATAACCA 1409  
QY 282 ProMetProProAsnGlnInProGlnThrThrSerValLeuIleArgLysThrAlaLeuGly 301  
Db 1410 -----RACCCPAAT-----ArgLeu 1418  
QY 302 AspTyrSerLysLeuLeuGluGlyAlaThrLeuGlnLeuThrGlyAspAsnValAsnSer 321  
Db 1419 -----TCAGACGCTGAGAAGGGTTTATGGTGAGTCGGGGAGAGCTG----- 1466  
QY 336 IleGluLeuSerAspGlyThrTyrThrLeuThrGluLeuAsnSerProAlaGlyThrSer 355  
Db 1521 CGGACACAAACGACACAACTCTGCCACAAACGGTTAGTTAGTCAGGCTTGAA 1580  
QY 356 IleAlaGluProLeuThrPhelysValGluAlaGlyLysValTyrThrIleLeuAspGly 375  
Db 1581 -----ANACCTAGCACCAAGGTTGTTGAGATAATGAAACGATGIGCAGATTAACAGC 1634  
QY 376 LysGlnIleGluAsnProAsnLysGluIleValGlu-----ProThrSerVal 391

Db 1635 AAAAGTTAACATGATGCGGTGATGAGAAATTGATAATGGGTGATATTCCCTACAGTG 1694  
QY 392 GluAlaTyrAsnAspPhe-----GluGluPheSerValLeuThrThr 405  
Db 1695 GAAAGCTATGAGTAATTCCTTGGGGAAAAAAGCAGATTCCCAAAAAGCAGC 1754  
QY 406 GlnAsn-----ArgLeuThr 406  
Db 1755 AGCAGCACCAGCGGCCAGCTATTGGCCAGATGATAATTTATTT 1808  
QY 415 AspLysAsnGlySerSerGlnAlaValThrCysPheAsnAlaAspLeuLysSerPro 435  
Db 1809 -----CATGGCAACTATATGACTATCAGCTACGCGAGCTGTGATAATGGCCCTGCC 1862  
QY 436 AspSerGluAspGlyGlyLysThrMetThrProAspPheThrThrGlyGluVal 453  
Db 1863 GATGCTGCAAGCCACCCATCTTAAGAAAATACCCAAATGCCACACTTAATAAG 1922  
QY 453 -----ArgLeuThr 453  
Db 1923 GACACCAAGTTACGCCATCTGCTACAAGAGGCCAAAGATAATAAGCCTTATACGCC 1982  
QY 454 -----LysThrThrIleAla-----GlyArgAspLeu-----ArgLeuThr 464  
Db 1983 ATTGCTGCCAAAGCTATCAGCACATCAGTTGGCGAGACGCTGTATAACGATGCCAAC 2042  
QY 465 -----LysThrThrValLysProArgAspThrAspProAspThrPheLeu 479  
Db 2043 CAAACCCAAACAGCAGSUTATTGTCGACGCCAGATACAGGCCACCGCTG 2102  
QY 480 LysHistLeuLysValLeu-----ArgLeuThr 486  
Db 2103 CCCAAGGGCATGAAATCACTTACAAACGGCTTGGCCAGGTATCTTATCCAAAMAAG 2162  
QY 487 GluLysGlyTyrArgGluLysGlyGlnAlaLeuGluThrSerGly 501  
Db 2163 GACAAGCTTATGCAATAATGAGAAACCCTAACAGAAAAAGGCCATCAAGATATCTG 2222  
QY 502 LeuThrGluThrGlnLeuArgAlaAlaThrGlnLeuAlaLysThrPheThr 519  
Db 2223 TPAACCGAGA-----ArgLeu 519  
QY 520 -----AspSerAlaGluLeuAspLysAspLysLeuLysAspTyrHisGlyPhe 535  
Db 2247 GATGATGAGCATGATGTTGACCGCCTGATGATGTTACAAAGATGATGATGACATGGCGAT 2306  
QY 536 GluAspSerAspSerThrIleLeuAlaValAlaLysIleLeuValGluThrAlaGlnAsp 555  
Db 2307 GATGATG-----ArgLeu 555  
QY 556 SerAsnProProGlnLeuThrAspLeuAspPhePheIleProAsnAsnLysThrGln 575  
Db 2340 GATGACCGAGATGGGGTGACGCTAGATGATGTTG-----GGTGATGTCAGATGAC 2393  
QY 576 SerLeuIleGlyThrGlnIlePheAspLeuValAspIleLeuArgMetGluAsp 595  
Db 2394 GCGCCGCGAGGCAAGCTATCATGCAGGTAT-----ATTCGCCTGAAATT 2441  
QY 596 LysLysGluValIleProVal-----ThrHisAsnLeuThrIleLeu 608  
Db 2442 GAAACAATACATGTCGCCATTATGAGCTACTCATGAAAGAACCTTGGCCTAGATGGT 2501  
QY 609 -----ArgLysThrValThrGlyLeuAlaGly 617  
Db 2502 AAAATAAGCTAAGTTGATGTTGAGTTTGACACCAACACGCTTAAGTAAATTAAC 2561  
QY 618 AspArgThrLysAspPheHisPheGluIleGluLeuLysAsnAsnLysGlnGluLeu 637  
Db 2562 GTGAGAGAGGCTGATCTGCTCTGATAC-----AAAATGGCAAAATGATGCGACA 2615  
QY 638 SerGlnThrValLysThrAspLysThrAsnLeuGluPheLysAspIlyLysAlaThrIle 657



OY . 302 AspTyrSerLysLeuIleGluGlyAlaThrLeuGlnLeuThrGlyAspAsnValAsnSer 321  
 ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 1419 -----TCAGACACGCCTGAAGCGGGTTTATGGTGAGTCGGCGATGAGCTG----- 1466  
 |||  
 OY 322 PheGlnAlaArgValPheSerSerAsnAsp 335  
 ||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 1467 -----GGGGTAATTCTTATCCAATGACAACGCATCTTATGGCTTGTGCTTGTGAA 1520  
 |||  
 OY 336 IleGluLeuSerAspGlyThrThrLeuIleGluAsnSerProAlaGlyThrSer 355  
 :::: :||| :||| :||| :||| :||| :||| :|||  
 Db 1521 CGAGCACAAACAGCACACCTCTGCCAACAAACGGTTATTAGCCAGGCTTGA 1580  
 |||  
 OY 356 IleAlaGluProIleThrPhenylAlaGluAlaGlyIysValTyrrThrIleAspGly 375  
 :::: :||| :||| :||| :||| :||| :||| :|||  
 Db 1581 -----AACCTTGACACCACTTGCTGAGATAATGAAACGATTTGGCAGAATTAAACGC 1634  
 |||  
 OY 375 LysGlnIleGluAsnProAsnIleGlu-----  
 ||| :||| :||| :||| :||| :||| :||| :|||  
 Db 1635 AAAAGGTTAAATGATGCGGGTGTAGAGAAAATGATAATGGGATATTCCCTAACAGT 1694  
 |||  
 OY 392 GluAlaTyrrAsnAspHe-----  
 ||| :||| :||| :||| :||| :||| :||| :|||  
 Db 1695 GAGCCTATGTTGAATTCCTGGGCGAAANAAAGCAGATTCCCCAAAGTCGC 1754  
 |||  
 OY 406 GlnAsn-----  
 ||| :||| :||| :||| :||| :||| :||| :|||  
 Db 1755 AGCAGCACCAAGCCGCGCACCTATTGGCAACATGATAATTATTTATTT 1808  
 |||  
 OY 416 AsnLysAsnGlySerSerGlnAlaValTyrCysPheAsnAlaAspLeuIysSerPro 435  
 ||| :||| :||| :||| :||| :||| :||| :|||  
 Db 1809 -----ATGGCAACTTATGACCTATGACCTATGACGAGCTGTTGATAATTGGCCC 1862  
 |||  
 OY 436 AspSerGluAspGlyGlyIysThrMetIleProAspPheThrThrGlyGluVal----- 453  
 ||| :||| :||| :||| :||| :||| :||| :|||  
 Db 1863 GATGCGTCAAGCCACCAAACTTAAAGAAATTACCTTAATGCCACACTAAATAG 1922  
 |||  
 OY 453 -----  
 |||  
 Db 1923 GACAACCAAGTTCGGCCATCGCTGCTAACAGAGAACATAAAAGCTTATACGCC 1982  
 |||  
 OY 454 -----LysThrThrIleAla--GlyArgAspLeuHe-----  
 ||| :||| :||| :||| :||| :||| :||| :|||  
 Db 1983 ATTCGTGCCAAAGCTATCAGCACATCAGTTGGCGAGACGCCTGTATAACGCC 2042  
 |||  
 OY 465 -----LYSTYrThrValLysProArgAspThrAspProAspThrPhel 479  
 ||| :||| :||| :||| :||| :||| :||| :|||  
 Db 2043 CAAACCCAACACGCACTATTGGCAAGGGAGATACAGCAGGCTG 2102  
 |||  
 OY 480 LysHistidineLysValle-----  
 |||  
 Db 2103 CCCAAGGCCAGGTAAATCACTTACAACGGCTTGGCAGGCTATCTTACCAAAAG 2162  
 ||| :||| :||| :||| :||| :||| :||| :|||  
 OY 487 GluLysGlyTYArgGluLysGlyGlnAlaLeuIlyrSerGly-----  
 ||| :||| :||| :||| :||| :||| :||| :|||  
 Db 2163 GACAAGGCTTATGCAATATGAGAACCATCAAGAAAGGCCATCAAGATATCTG 2222  
 |||  
 OY 502 LeuThrGluThrGlnIleArgGalaAlaThrGlnIleAlaIleItyrThrHe----- 519  
 ||| :||| :||| :||| :||| :||| :||| :|||  
 Db 2223 TPAACCCAGAC-----  
 |||  
 OY 520 -----AspSerAlaGluLeuAsnIysAspIysLeuLysAspTY-HisGlyPhe 535  
 |||  
 Db 2247 GATGATGACGATGATGTTGGCCATGTGATGATCACAGATGATGCACTGGCGAT 2306  
 |||  
 OY 536 GlyAspMetAsnAspSerThrIleAlaIleAlaValIleAlaValGluTYAlaGlnAsp 555  
 |||  
 Db 2307 GATGATGTTG-----  
 |||  
 OY 556 SerAsnProProGlnIleAspPhePheIleProAsnAsnAsnLysIysGln 575  
 |||  
 Db 2340 GATGACGCCAGTGGCGATGAGCATGATGATGTTG-----GGTATGGCAGATGAC 2393  
 |||  
 QY 576 SerLeuIleGlyThrGlnInTrpHisProGluAspLeuValAspIleArgMetGluAsp 595  
 :::: :||| :||| :||| :||| :||| :||| :|||  
 Db 2394 GCGCCGCAAGGCAAAGTATCATGCAGTAAT-----ATTGCCCTGAATT 2441  
 |||  
 OY 596 LysLysGluValleProval-----ThrHisAsnLeuThrIle----- 608  
 :::: :||| :||| :||| :||| :||| :||| :|||  
 Db 2442 GAACACAAATACCTTGCCCATATGAGCTACTCTATGAAAAACCTTGCCCTAGATGGT 2501  
 |||  
 OY 609 -----ArgLysThrValThrGlyLeuAlaGly 617  
 :::: :||| :||| :||| :||| :||| :||| :|||  
 Db 2502 AAATAAGCTAAGTTGATGTGATTTGACACCAACAGCCTAATGGPAATTAAAC 2561  
 |||  
 OY 618 AspArgThrLysAspPheHisPheGluIleGluLeuIysAspAsnIysGlnGluLeu 637  
 |||  
 Db 2562 GATGAGAGGAGGATATGCTCTTGATATC---AAAATGCCAAATTGATGGCACA 2615  
 |||  
 OY 638 SerGlnThrValLysThrAspIysThrAspIleGluIleGlyAspGlyIysAlaThrIle 657  
 |||  
 Db 2616 GCCTTACCGCCAAAGCGATGNGCACAATCTGCAAGAAGTGGCT----- 2663  
 |||  
 OY 658 AsnLeuIyshisGlyIuSerLeuThrIleGlyLeuProGluGlyTySerIyLeu 677  
 |||  
 Db 2664 AACACCAAGGCGC-----  
 |||  
 OY 678 ValIysGluThrAspSerGluGlyTyIysValAsnSerGlnGluAla----- 696  
 :::: :||| :||| :||| :||| :||| :||| :|||  
 Db 2694 ATCAAGATATGTCAGGCAAACTTGTGCAACATGGGCAATTGCGACAATGGCGAGAGTGTGCAAGGG 2753  
 |||  
 OY 697 -----  
 |||  
 Db 2754 CAGTACAGTACGACAAGGGATGGCATCAATGACACGCCGAAAGCAGGG 2807  
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 RESULT 6  
 US-09-074-658-69  
 ; Sequence 69, Application US/09074658  
 ; Patent No. 6104371  
 GENERAL INFORMATION:  
 APPLICANT: Loosmore, Sheena M  
 APPLICANT: Run-Pan Du  
 APPLICANT: Quilun Wang  
 APPLICANT: Yang, Yan-Ping  
 APPLICANT: Klein, Michel H  
 TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA  
 NUMBER OF SEQUENCES: 78  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Sim & McBurney  
 STREET: 6th Floor, 330 University Avenue  
 CITY: Toronto  
 STATE: Ontario  
 COUNTRY: Canada  
 ZIP: M5G 1R7  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC DOS/MS DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/074, 658  
 FILING DATE: 08-MAY-1998  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Stewart, Michael T  
 REFERENCE/DOCKET NUMBER: 1038-795  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (416) 595-1155  
 TELEFAX: (416) 595-1163  
 INFORMATION FOR SEQ ID NO: 69:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 218 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear

US-09-074-658-69  
Alignment Scores:  
Pred. No.: 2.12e-08 Length: 2718  
Score: 176.00 Matches: 164  
Percent Similarity: 33.42% Conservative: 102  
Best Local Similarity: 20.60% Mismatches: 264  
Query Match: 4.468 Indels: 266  
DB: 3 Gaps: 40

US-09-494-297-2 (1-757) x US-09-074-658-69 (1-2718)

QY 84 TyrTyrylrgInPheArgValAlaHisAspLeuArgValAsnLeuGluSerArg 103  
Db 493 TATTGATGATAATGCCCAAATATCCGAGCTG---CACCTAGAACAGCGG--- 543

QY 104 TyrGlnValTyrCysPheAsnLeuLysLysAla-----PheProLeuGly 118  
Db 544 -----CATGCTTTGATGCTAAAAGCAAAATACATCAAATATATGGCTATGGT 594

QY 119 SerAspSerSerValLysLys-----TrpTyrylrsLysIaspGlyLys 133  
Db 595 GCATGTCATCACCTGCCAAAACCCAACTACATGAATATCACACAGAACAC 654

QY 134 SerThrLys-----PhcGluAspPyroAla-----MetSerProArg 145  
Db 655 AAAACAAAAACAGGCAGGCGATGATTAATCACAAACATCGTTGGCTATAGGAGCTAAGA 714

QY 146 IleThr-----GlyAspGluLeuAsnGlnLysLeuIrgAlaValMet 159  
Db 715 GAGCAGGACCTAAATAAAAGGAGCAGACCCAGAGCACAGAACGCGCATCATT 774

QY 160 TyrAsnGly-----HisProGlnAsnAlaAsnGlyIleMetGluGlyLeu 174  
Db 775 TTACACCACACTACTTATTTATCATGGGAGAATGCGCAGCACCATGTGCCA----- 828

QY 175 GluProLeuAsnAlaIleArgValThrGlnGluAlaValTrpTyrylrsAspAsnAla 194  
Db 829 -----AAGGGGGTAAATTGACTATGAGGGCAATTGGTGATCTGACCGATGTC 879

QY 195 Pro-----IleSerAsnProAspGlu-----SerPhe 203  
Db 880 AAAAACGCCATTAGATAAAACAGAGATAAAGTAGGACATTATTAACTCAAC 939

QY 204 LysArgGluUserGluSerAsnLeuValSerThrSerGlnLeuSerLeu 219  
Db 940 AGAAATCAGATGAGGCCATTGGTGGACTGCGCACACATTCTAACAGCTTAA 999

QY 220 -----MetArgGlnAla 223  
Db 1000 TATAACACACCCGGCCACTATAGCGTGACTTGTATCAAATACCTAAAGGCAA 1059

QY 224 LeuIysGlnIleIleAspProAspLeuAlaThrIlysMeProLygSlnValProAspAsp 243  
Db 1060 TIGCTTATATGACACCCAAACAGCAACAGCGGATGGCGTTATTCAGAGTCG 1119

QY 244 Phe-----GlnLeuSerIlePheGluUserGluAspLys----- 254  
Db 1120 TTGTGATCAGCACAAGGCTCAATGAGCGGATGCTAGAGATGACGCCAGATTAA 1179

QY 255 GlyAspLysTyrAsnLysGlyTygGlnAsnLeuLeuSerGlyGlyLeu----- 270  
Db 1180 GGCACACGCCCTACTGGCACAGCCAAATGTTGATGATAACACCATACCGCACCT 1239

QY 271 -----ValProIlysProProThrProGlyAspProProMetProProAsn 286  
Db 1240 TTGTTAAAGAGCTTCCTCAAAAGCAATCCACACACCA-----GACCCAC 1293

QY 287 GluProGlnIthrThrSerValLeuIleArgLysTyrAlaIleGlyAspTyrSerIlysLeu 306  
Db 1294 -----TCAGATAGC 1302

QY 307 LeuGluGlyAlaThrLeuInLeuThrGlyAspAsnValAsnSerPheGlnAlaArgVal 326

Db 1303 CTAGAGGGGTTATGGTGAATGGGGATGAGCTG-----GCGGTTAA 1350  
Qy 327 PheSerSerAsnAspIle-----GlyGluArgIleGluLeuSer 339  
Db 1351 TTTTATCCATGACAAACGCAACTTTGGTGTCTTGGGCAACGAGACAAACGACC 1410  
Qy 340 AspGlyThrTyrylrsLeuIrgLleuAsnSerProAlaGlyTyrsSerIleAlaGluPro 359  
Db 1411 GAACCTGTCGCCACAAACGGTGTATTAGT-----ACAGGATTTGAA-----AACCC 1461  
Qy 360 IleThrPhelysValGluAlaIgylsValTyrylrsValTyrylrsIleIleAspGlyLys----- 376  
Db 396 AspPhe----- 405  
Qy 377 ---GlnIleLysAspProAspLysSglLeuValGluIuprotYrsSerValGluAlaTyrsn 395  
Db 1522 GATGAGTCATAAACAACTAACTGAAACTGCGCCGTCATAATAAAGATAAT 1581  
Qy 406 GlnAsnTyrla-----LysPheTyryr----- 413  
Db 1642 AAAACCCCTATTTGGTCAGCATGATAAGTTTAAATGGTAACTATTATGAC 1701  
Qy 414 -----AlaYs-----snyAsnGlyIleSerGlnValValTyrcyPheAsnAla 429  
Db 1702 TTATGCGCCTAAAGAACAGCAACAACTAACAAATAACGCCAGCCAACTAAAGAT 1761  
Qy 430 AspLeuIysSerProProAspSerGluAspGlyGlyLysThrMetThrProAspPheThr 449  
Db 1762 ATTGGCTAAATACCGAGATGCC-----AAAGTAAGCAGACAATAAAGT 1809  
Qy 450 Thr----- 450

Db 1810 ACCAAATCCTCTCACACAGCAAAAGATAAGCCGATACGCCATTATGCCAAAGC. 1869  
Qy 451 -----GlyGluWlyLysTyrHrHsileAlaIgylsArgAspLeuPhe 464  
Db 1930 AGTTATTGTCAGGCGGTCAAGCGGATGTCAGTACAGCAGGCCAGTSCAGGTAA 1989  
Qy 481 -----HistIlysLysValIleGluLysGlyTyryarg 491  
Db 1990 TCACCTATATGCTCTTGGCAGGCTACCTGACCCAGAAAAAGACAAAGTTATGC 2049  
Qy 492 GluIysGlyGlnAlaIleGluTyryserGlyLeuIrgLleuGlnLeuIrgAlaAlaThr 511  
Db 2050 AAAGATGAGGATACCATCAGCAAAAGGCTTAAAGAT----- 2088  
Qy 512 GlnLeuAlaIleTyryrPheThr----- 519  
Db 2089 -----TANATATGACCAAGACTTTACCCACAAGATGACGATGACGATGAC 2136  
Qy 520 AspSerAlaGluLeuAspLysAspLysLeuLysAsp-----TyrHsGlyPheGlyAspMet 538  
Db 2137 GATAGTTGACCGCATCTGATGATGATCACAGATGATAATCACATGGGGATGATGATG 2196  
Qy 539 AsnAspSerThrLeuAlaValAlaLysIleLeuValGluTyralaGlnAspSerAsnPro 558  
Db 2197 -----ATTGATCTGTGATGATCACAGATGATGAC 2229  
Qy 559 ProGlnLeuThrAspLeuAspPhePheIleProAsnAsnAsnLysTyrGlnSerIleUrle 578  
Db 2230 GATGCGATGACGATTCAGATGATGATG-----GGTGATGTCAGATGATGCCCA 2283  
Qy 579 GlyThrGlnTrpHsProGluAspLeuValAspIleArgMetGluAspLysLysGlu 598

Query Match: 4 .08% Indels: 166  
DB: GCAAACTGTATCATGCAGGTAAT-----ATTGCCCTGAATTGAAACAAA 2331  
Qy 599 ValIapproval-----ThrHisAsnLeuThrLeu----- 608  
DB 2332 TACTGCCATTAAATGAGCCTACTCATGAAACACCCATTGCCCTAGATGTTAAATAAG 2391  
Qy 609 -----ArglysthrValThrGlyLeuAlaGlyYASPAGThr 620  
DB 2392 GCTAAGTTGTGTAACATGACACACAGCCTACTGGTAATAACGATGAGAGA 2451  
Qy 621 LYSASPPHeHISphegluilegluleutlysasnlysGlnGluLeuSerGlnThr 640  
DB 2452 GGTGAAATCGCTCTGATAC-----AAAGATGGCAAATTGATGCCACAGGATTAC 2505  
Qy 641 ValysthrAspLysIleLeuGluPheAspGlyLYSAlaThrIleAsnLeuLys 660  
DB 2506 GCCAAAGCGATGTCGCAACPATCGTGAAGAAGTGGGT-----AACAAACAA 2553  
Qy 661 HISGYVGLuSerLeuThrLeuGlnGlyLeuProGluGlyYrSerTyrlLeuValLysGlu 680  
DB 2554 GGTGGC-----GGTCTCTATACACATCAAGAT 2583  
Qy 681 ThrasPSerGluGlyTyrylLysValasnSerGlnGluValAla 696  
DB 2584 ATTGATCTAAGGGCAATTGTCGACAAATGGCAAGAGTTGGCA 2631  
RESULT 7  
US-09-071-035-403  
; Sequence 403, Application US/09071035  
; GENERAL INFORMATION:  
; APPLICANT: Gil H. Choi  
; TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides  
; NUMBER OF SEQUENCES: 495  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: Maryland  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Disquette, 3.50 inch, 1.4Mb storage  
; COMPUTER: HP Vectra 486/33  
; OPERATING SYSTEM: MSDOS version 6.2  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/071,035  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: A. Anders Brookes  
; REGISTRATION NUMBER: 36,373  
; REFERENCE/DOCKET NUMBER: PR369P2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (301) 309-8504  
; TELEFAX: (301) 309-8512  
; INFORMATION FOR SEQ ID NO: 403:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4249 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-09-071-035-403  
Alignment Scores:  
Pred. No.: 1.72e-06 Length: 4249  
Score: 161.00 Matches: 159  
Percent Similarity: 34.83% Conservative: 104  
Best Local Similarity: 21.06% Mismatches: 326  
Query Match: 4 .08% Gaps: 40  
DB: GCAAACTGTATCATGCAGGTAAT-----ATTGCCCTGAATTGAAACAAA 2331  
Qy 39 AlaLeuValThrSerMetValGlyAlaLysThrValPheGlyLeuValGluSer----- 56  
DB 1451 TCATTAAGTACACCTGTAATGCTCCFAATAAAGCCATTCAATTGATGATCATAAT 1510  
Qy 57 --SerThrProAsnAlaLeuIleAsnProAspSerSerSerGlyUtyArgTrpGlyYr 75  
DB 1511 ATTGACCAATTGTCGTTGTTGTT-----TIGAATGCTGAACTCTGGTATTAT 1567  
Qy 96 -----valAsnLeuGluGlyYrSerArgSerTyrlGlnValTrpCysAsnLeuLysLys 113  
DB 1595 ACAACTCTCTCAGTATGGAGAACGATTCAAAATTAGAAATTAAGTA 1654  
Qy 114 AlaPhePro-----LeuGlyYrSerAspSerSerValLysLystpTyrylLysLys 129  
DB 1655 AACATCTAAATCTCTTCATTCAGCTAACAAAGAAATTATTATTTATCACAG-- 1711  
Qy 130 HisAspGlyYrSerThrLysPheGluAspTyralMetSerProArgIleThrGlyAsp 149  
DB 1712 -----TIGGAGC-----GATTTACAGTAAGGCCAACGTCAGATGGTCA 1753  
Qy 150 GluLeuAsnGlyLysLeuArgAlaValMetYrAspGlyHisProInAspAlaLysGly 169  
DB 1754 GTTTAAAGTCACATGCCATAACCAACGAAATCCAATGGTTATTAT 1813  
Qy 170 IleMetGluGlyLeuGlu-----ProLeuAsnAlaIleArgValThrGln 184  
DB 1814 GTCGCAAGTAGTGTGCAAAGATAAAAGATCCATGCAACGATACCGATAATG 1873  
Qy 185 GluAlaValTrpTyryrSerAspAsnAlaProleSerAsnProAspGluSerPhelys 204  
DB 1874 AGTCGTAAGGTTAACTCCAGTTGATACGAGCACTRACT-----ARTGAAAG 1924  
Qy 205 ArgGluSerGluSerAsnLeuValSerThrSerGlnLeuSerLeuMetArgGlnAlaLeu 224  
DB 1925 CGTGGTCTGACGAACACTCAAAAGTAGAAATCAATTCATCTGCAATGCGACAAT 1984  
Qy 225 LysGlnLeuIleAspProAsnLeuAlaThrLysMetProLySglnValProAspSphe 244  
DB 1985 GATTCTTTGACTCACTAAAGGTCCTACACAATTCAGCTGGGCC-----CATGT 2038  
Qy 245 GlnLeuSerIlePheGluSerGluAspLysGlyAspLysYrAsnLysGlyTyrglnAsn 264  
DB 2039 CTTTGACATTTGATGTTCAAC-----GATCAGGTTGATGCAATTATCCACAA 2092  
Qy 265 LeuLeuSerGlyGlyLeuValProThrLysProProThrProGlyAspProProMetPro 284  
DB 2093 TACTGGGACCGCGGTCAACTTGTAAACCAATGACGCCAAACAGCCCCTGGATATCCA 2152  
Qy 285 -----ProAsnGlnProGlnThrThrSerValLeuIle-----Arg 296  
DB 2153 ACGATTAATTTGACGAAATACTTACCAATGACGTTACACGTTGAAACACACAA 2212  
Qy 297 LYSTYAlaLeuGlyAspTyryrSerLysLeu-----LeuGluGlyAlaThrIleGln 313  
DB 2213 CGTTACATTAT-----GAGTATAAAAGGCCAATGCGTGGATGCGCACTCTTAT 2269  
Qy 314 LeuThrGly-----AspAsnValAsnSerPhiGlnAlaArgYrAlpHe 327  
DB 2270 ATTCAGGGACAGCGGAAAGAACCACTGATAATAATGAGGTCTGCITCGTTCT 2329  
Qy 328 SerSerAsnAspIleGlyGlyIleGluLeuSerAspGlyIleThrYrThrLeuIleGlu 347  
DB 2330 GTTCAAAT-----GAAGCTTGAGACATTGTCGAAACA----- 2365



Db	1663 GATCAA-----AAATGGTGCCTATTGTCATCAGA	1689	Qy	425 TYFCYSpheAsnAlaAspIeulySSerProProAspSerGluAspGlyGlyLysThrMet 444
Qy	96 -----ValAsnLeuGluGlySerArgSerTyrGlnValTyrcySPheAsnLeuLys 113		Db	2635 T-----TCATTAGAGAGACTACAAACGGTGCGAMAGTCATT 2673
Db	1690 ACAAATGCTCACTTATGCGGAGCAAGAGAACCGATTCAAAATTAGAAATTAAAGTA 1749		Qy	445 ThrProAspPheThrThrGlyIu-----ValysTyrThrHisIleLeuGlyArg 461
Qy	114 AlaPhePro-----LeuGlySerAspSerSerValysLysLys 129		Db	2674 TTTAAAGACTATCACATGAGCTACAAAGAAATTATTATTAACAG--- 1806
Db	1750 AACATCTTAATTATCTTCATACGAGCTACAAAGAAATTATTATTAACAG---		Qy	462 AspLeuPheLysTyrThrValysProArgPheAspProAspIeulySerProArgIleLeuGlyAsp 149
Qy	1330 HISAspGlyIleSerThrLysPheGluAspPheSerValysPheGluAsp 149		Db	2734 GCIGGCCAACATCIRACAAACACATGACTGACATTTGACAGATGTCGCT 2793
Db	1807 -----TIAAGAACG-----GATTAATACAGAACGCCAACG 1848		Qy	482 IleLysIvvalle-----GluLys 488
Qy	150 GluLeuAsnGlyLysLeuArgAlaValMetTyrAsnGlyHisProGlnAsnLysLys 169		Db	2794 AGCAAGAAAAAGCACCCTGCGCCAACTCACATGAAATTCTCGAGGTGCGGA 2853
Db	1849 GTTATAAGTCACTACGCCAAATACCAACAGAACATCCAAATTCCAATTTGTTTAAT 1908		Qy	489 GLYTYRAGLunysGIVlnAlaIleGluTyrSerGlyLeuThrGluThrGluLeu 508
Qy	170 IleMetGluGlyLeuGlu-----ProLeuAsnAlaIleArgValThrGln 184		Db	2854 GGTTTTGTTTATTTAGCACTGOCACANTCTACACGCAAACTACGCAAACTGAGGATGACAA 2913
Db	1889 GTGCCAGATAGTTGCCCCAAAGATAAAGTATCCACTGATACGATACCGATAACATG 1968		Qy	509 AlaAlaLysGluLeuAlaIleLeuLysTyrPheThrAsp-----SerAlaGluLeu 524
Qy	185 GluAlaValTrpTyrTyrSerAspAsnAlaProIleSerAsnProAspGluSerPhens 204		Db	2914 GCATTGGAAAGCTTCTTGAECTTGTACTTGTGACATGTCACGCAACGGATT 2973
Db	1969 AGTCTGAGGTTTACCTCCAGTGTACAGTACTA-----ATTAGTAAAG 2019		Qy	525 AspLysAspLysLeuLysAspTyrHisGlyLysAspMet---AsnAspSerThrIeu 543
Qy	205 ArgGluLysGluSerAsnLeuValSerThrSerGlnAlaLeu 224		Db	2974 ACACAGATGAAAGGICAACTACTCCCTTGACTTGTGCCATCATGACGGGTGATTTG 3033
Db	2080 GATCTTTGACTCACTGACGTCGTCGTAACAGATGAAATTGAAAT 2079		Qy	544 AlaValAlaLysIleLeuAlaIleLeuLysTyrPheThrAsp-----AspLeuPhePheIlePro 562
Qy	225 LysGlnIleLeuAsnProAsnLeuIalThrLysMetProLysGlnValProAspAspHe 244		Db	3034 CGACTAACGAAATGACCGCAGGATAATTCCGCTGGATGAGAG---TATTGACAGGA 3087
Db	2188 TACTGGGACCGGGTCAACTTGTATAAACCAATGAGGCCAACAGCCCTGGATATC 2247		Qy	563 -----AspLeuAspIleLeuIleValGluTyrAlaGluAspSerAspProProGlnIleThr--- 569
Qy	2314 CTTTTGACATTTGATGTTCAAC-----GATCGGTAGATTCATTATC 2187		Db	3088 AAACCCATTAAGCIGGTCAAAGGAGCACCAACTAAATTAACGAAACATT 3147
Qy	255 LeuLeuSerGlyIleLeuValProThrLysProProThrProProLysAspProProMetePro 284		Qy	570 AsnAsnAsnLysLysTyrGln-----SerIleLeuGlyIleLeuLysTyrGlnTrpHisPro 584
Db	2188 TACTGGGACCGGGTCAACTTGTATAAACCAATGAGGCCAACAGCCCTGGATATC 2247		Db	3148 GATCCACAGTCGTTTCAAGTCAAAGATTCACGCAAACTTGTCCGGATTCTCGAA 3207
Qy	285 -----ProAsnGlnProGlnIleThrSerValleuIle-----Arg 296		Qy	585 GluAspIleLeuAspIleLeuArgMetGluAspLysLys---GluValleuProValThr 603
Db	2248 ACCGATATTGACGAAATACCAATGCTGATTTGGAAAACCAAA 2307		Db	3208 GAAGAG-----ACTTTGTTGACACAGATAAACAGGTTCAGAGCTTCCCTTCGAA 3261
Qy	297 LysTyraIleLeuGlyAspTyrSerLysLeu-----LeuGluGlyAlaThrLeuGln 313		Qy	604 HisAsnLeuThrLeuArgLysThrValThrGlyLeuAlaGlyAspArgThrLysAspHe 623
Db	2308 CGTACATTTATT-----GAGTATAAACCCCAATGCTGATCCACTCTTAT 2364		Db	3262 -----AAATACGTTGTTGAGGTCAGTCAGGCTCAACTGATAACCAAGGGTT 3306
Qy	314 LeuThrGly-----AspAsnValAsnSerPheGlnAlaLeuGlyIleLeu 327		Qy	624 HisDpheGluIleLeuLeuLysAsnAsnTysGlnGluLeuLeuSerGlnIleLeuThrValLysThr 643
Db	2365 ATACAGGGACAGCGAAAGAACACACAATCGAATTAATAGAACGGCTCTGCTTGGTTCT 2424		Db	3307 TATCCCAATTATTTCAGTCAGCAGGAAGTAARGAACACGCCCTATGACGCCAAACC 3366
Qy	328 SerSerAsnAspIleGlyGluArgIleLeuSerAspGlyIleThrThrLeuGlu 347		Qy	644 AspIleThrAsnLeuGluIleLeuLysAspGlyIleAspIleLeuLeuLysIleGlyGlu 663
Db	2425 GTTCAAAAT-----GAAGCTTAGCATTTGATGTCACAA 2460		Db	3367 GACCAATTCATTAAGTCTAGGTCACAGAT-----ACACGATTTGTTGGGT 3414
Qy	348 LeuAsnSerProAlaGlyTyrSerIleLeuAlaGluProIleThrPhelysValGluAlaGly 367		Qy	664 SerIleThrLeuIleGlyIleLeuProGluGlyIleTyrSerIleLeuValLysGluThrAspSer 683
Db	2461 -----CAAGCGCGAATCCACACATAAATGTAACAAACG 2499		Db	3415 TCGGGAAA-----GATATTGCTTCTGAGCAGACAAA 3456
Qy	368 LysValTyrThr-----IleIleAspGlyIys-----GlnIleGluAspProAsnLysGlu 384		Qy	684 GluGlyIleLysVal-----LysValAsnSerGlnGluValAlaAsnAlaThrVal 700
Db	2500 ACAGTAAACAAACAAAAATATTGATAATAAACACATCGTGTGAAACAAACGATGAA 2559		Db	3457 ACAGGTCAAGACGCTTNCGGTTGAAAKATGTGTCGGAAACAGTGAAT----GTT 3510
Qy	385 IleValGluProTyrSerValGluIleTyrAsnAspGluGluPheSerValleuLeuThr 404		Qy	701 SerIleGlyIleIleSerAspGluIleLeuAlaPheGluAsp 715
Db	2560 TTACACCAAAAGCACAACCAATGCTCAATGCTGAAATCTACCGCG----- 2613		Db	3511 GATAAAATAGGC-----GATATGAATGTCATAAAAT 3546
Qy	405 ThrGlnAsnTyrAlaLysPheTyrTyrAlaLysAsnAsnGlySerSerGlnValVal 424		RESULT 9	US-08-531-567B-48
Db	2614 -----AAAGCGTCCAGAGATCT 2634			; Sequence 48 Application US/08851567 ; Patent No. 6528484

## GENERAL INFORMATION:

APPLICANT: Ensign, Jerald C  
 APPLICANT: Bowen, David J  
 APPLICANT: Petel, James  
 APPLICANT: Ratig, Raymond  
 APPLICANT: Schoopover, Sue  
 APPLICANT: ffrench-Constant, Richard  
 APPLICANT: Rocheleau, Thomas A.  
 APPLICANT: Blackburn, Michael B.  
 APPLICANT: Hey, Timothy D.  
 APPLICANT: Merlo, Donald J.  
 APPLICANT: Orr, Gregory L.  
 APPLICANT: Roberts, Jean L.  
 APPLICANT: Strickland, James A.  
 APPLICANT: Guo, Lining  
 APPLICANT: Cliche, Todd A.  
 APPLICANT: Sukhapinda, Kititsri  
 APPLICANT: Orr, Gregory L.  
 NUMBER OF SEQUENCES: 88  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: Dow AgroSciences Patent Department  
 STREET: 9330 Zionsville Road  
 CITY: Indianapolis  
 STATE: IN  
 COUNTRY: US  
 ZIP: 46268  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patient Release #1.0, version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/851, 567B  
 FILING DATE: 05-MAY-1997  
 CLASSIFICATION: 514  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 08/063, 615  
 FILING DATE: 18-MAY-1993  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 08/395, 497  
 FILING DATE: 28-FEB-1995  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 60/007, 255  
 FILING DATE: 06-NOV-1995  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 08/608, 423  
 FILING DATE: 28-FEB-1996  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 08/705, 484  
 FILING DATE: 28-AUG-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Seay, Nicholas J  
 REGISTRATION NUMBER: 27386  
 REFERENCE/DOCKET NUMBER: 960295, 93804  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 608-251-5000  
 TELEFAX: 608-251-9165  
 INFORMATION FOR SEQ ID NO: 48:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 5547 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 US-08-851-567B-48

Alignment Scores:  
 Pred. No.: 2.4e-05  
 Score: 152.00  
 Percent Similarity: 33.13%  
 Best Local Similarity: 18.29%  
 Query Match: 3.85%

Length: 5547  
 Matches: 148  
 Conservative: 120  
 Mismatches: 287  
 Indels: 254  
 Gaps: 37

US-09-494-297-2 (1-757) x US-08-851-567B-48 (1-5547)

QY 157 AlalvalMettryAspGlyHisProGlnAsnAlaasnGlyileMetGluGlyLeuGluPro 176  
 Db 2386 GCACACAATGAGTGCGCCACAGGGTTCGCGTTGGC--GGCGGATAT 2442  
 QY 177 LeuAsnAlaileArgValThrGlnIu--AlaValTrpTrpTrpSerAsp----- 192  
 Db 2443 ATTCATCATGAAAGAGACCGAACCTATGCCAGTGGAAAACGGCAGGGTATA 2502  
 QY 193 -----AspAlaProIserAsnProSpGluSerPheLysrgGluSerGu 208  
 Db 2503 ACCGCGGGTTGAATTCACACAGGCTAACTACATTACACGCTTTCGATGATCTCG 2562  
 QY 209 SerAsnLeuValSeThr-----SerGlnIeuSerLeuMetArgGlnAlaLeulys 225  
 Db 2563 AGTGCAGCAATTAGCCACCTATATCCGTCAGCAGCAGGCTATTAA 2622  
 QY 226 Gln-----LeuIleAspProAsnLeuAla----- 233  
 Db 2623 AGCCATGTGACTTGATCATACIATACGATGATGAAATCAGGITCTCGGGCAATAAA 2682  
 QY 234 ---TyrLysMetProLysGlnValProAspAspPheGlnIeu----- 246  
 Db 2683 ACCACCCGGATCAGGCCAGGCCATGCC---AGTATCAACTGTACCGGCATG 2739  
 QY 247 ---SerIlePheGluSerGluAspLysGly----- 255  
 Db 2740 GAAATAGTGTGAAAGAAATGCAATGGGGTTACAGCGCCRAATTCTTATCGGACTCG 2799  
 QY 256 AspLysTyRasnLysGlyTyrGlnasnLeuLeuUserGlyGlyLeuValProThrLysPro 275  
 Db 2800 GACAATACTACATAAACGCTACAGGACTTGGGGGGTGTCTCAAATTAGTTACTACCG 2859  
 QY 276 ProThrProGlyAspProProMetProProAsnGlnProGlnThrThrSerValLeuIle 295  
 Db 2860 GAAACTATATTGATCCGACCATGGCTATGGACAAACCAAATGATGGACGCCATRACTG 2919  
 QY 296 ArgLysTyrAla----- 299  
 Db 2920 CAATCGGTAGGCCAAAGCCAATTAAACGCCGATACCGTGAAAGATGCTTATGCTTAI 2979  
 QY 300 IleGlyAspTyrSerLysLeuLeuIleGluGlyAlaThrLeuGlnLeuThrGlyAspAsnVal 319  
 Db 2980 CTGACATCGTTGAAACAAGGCTGCTATCTTAAGTTATTAGCCATATCACGATAATANT 3039  
 QY 320 AsnSerPheGlnAlaArgValPhe-----SerSerAsnAspIleGlyGlu-- 334  
 Db 3040 AATAACGATCAAGGCTGACCATTTATGGACTCTAGTGAAGACTGangGCCGGAAT 3099  
 QY 335 -----ArgIleGluLeuUserAspGlyIleThrTyrThrLeuThr----- 346  
 Db 3100 TATGCCGCGAAGTGTGATCACGTAATCAACCAGGAAATGCCGCTTAATGCCCTG 3159  
 QY 347 -----GlueLeuAsnSerProIleGly-----TyrSerIleAlaGluProIle 360  
 Db 3160 AGTGATGGCATAAAATTGATGTCGCAATTAAACCTTATAAACCACTATCCGTCAGTG 3219  
 QY 361 ThrPheLysValGluIuIaglyLysValThrIle-----IleaspGlyLysGlnIeglu 379  
 Db 3220 ATATATAA-----TCCGGCTGTATCTGCTGTGAAACAAAGGAGGATCACC 3270  
 QY 380 AsnProAsnLysGluIleValGluIuIrotrySerValGluAlaItyrasnAspPheGlu-- 398  
 Db 3271 AACAGACAGGAATAGTAGAAGATGCTATCAAACGGAATATGCTTATGAACT 3330  
 QY 398 ----- 398  
 Db 3331 AAATGGCGCATATCGCTATGATGTCGACTTGGAAACGCCAATCACCTTGATGTCAT 3390  
 QY 399 --GluPheSerValLeuIleThrGlnasn-----TyrAlaLysPhe 411

Db 3391 AAAAATATCCGAGCTAACTGGAAAATAGAGCCCGACTCTATGTGCCGT 3450  
 Qy 412 TyrTyrAlaLysAsn----- 416  
 ||||| : : : : : : :  
 Db 3451 TATCAAGGTGAGATACTGTTGGTGATGTTTATACCAACAAGACACTAGATAGT 3510  
 Qy 417 ---LYSArgGlySerGlySerGlySerGlySerGlySerGlySerGlySerGlySerGlySerPro 435  
 ||||| :  
 Db 3511 TATAAACGCGTCAGCAGACTATATCTT---GCTGATATGCATCC----- 3561  
 Qy 436 AspSerGluAspGlyGlyLysThrMetThrPro----- 446  
 ||||| :  
 Db 3562 -----AAAGATAGACCCGAGAACAGCAAGTTATGGATAATACCGCTATGCAGAGGT 3603  
 Qy 446 ----- 446  
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 Db 3604 AGCTATCACAAATTGATACCAATAATGTCAGAAGAGTGAATAACGCCATTGCA 3663  
 Qy 447 -----AspPheThrThrGlyGluValLysTyr 455  
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 Db 3664 TATGAGATTCCTCCRGTAAGTAGCCGTAAGACTATGGTGGGAGATTACCTC 3723  
 Qy 456 ThrHistLeaLagLysArgAspIlePheLysTyrThrValAlaAspPheAspPro 475  
 ||||| : : : : : : :  
 Db 3724 AGCATGGTATAACGGAGATTCCACTACTAACATACAAAGCCCATCAAGTGTAA 3783  
 Qy 476 AspThrPheLeuLysHisIleLysLysValIleGlyLysGlyTyr-----Arg 491  
 ||||| :  
 Db 3784 AAATCTTATCTCACCAAAATTAAAGATAATTCTAAATGGATATGAGGACAAAGGC 3843  
 Qy 492 GluLysGlyGlnAlaLeuGluTyrSerGlyLeuThrGluThrGlnLeuArgLaAlaThr 511  
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 Db 3844 AACATCAATGCAAACTGATGAAATATGGCAACTAGGTGATAATTATGTTTATAC 3903  
 Qy 512 GluLeuAlaLeuTyrTyrPheThrAspSerAlaGluLeuAspLysAspLysLeuLysAsp 531  
 ||||| : : : : : : :  
 Db 3904 ACCTGGGGTCAATCCAATAACTGGTCAATGCTCATGTTACCCGICATCAA 3963  
 Qy 532 TyrHisGlyPheGlyAspMetAsnAspSerThrLeuAlaValAlaLysIleLeuValGlu 551  
 ||||| :  
 Db 3964 TATAGCCGA-----AACACGAGTGGACTCAATCAAGGGAGACTACTA----- 4005  
 Qy 552 TyrLysGlnAspSerAsnProBogInleuThrAspLeuAspPhePheIleProAsnAsn 571  
 ||||| :  
 Db 4006 TTCCACCGTGACCACTTATCCA-----ICTAAAGTAGAGCTGTTGATCCTGGAGCA 4059  
 Qy 572 AsnLys-----TyGlnSerLeuIleGlyLysThrGlnTrp----- 582  
 ||||| : : : : : : :  
 Db 4060 AACGTCTCTAACCAACCAAATGCCCATGGTGTATGCTACGACTCTG 4119  
 Qy 583 --HisProGluAspLeuValAspIleIleargMetGluAspLysLysGluValile--- 600  
 ||||| :  
 Db 4120 ATAAACCGGAGTGTCTAACAAATATCTTGTACTGACAGTAAAGGACTGCTACT 4179  
 Qy 601 -----ProValThrHisAsnLeuThrLeu-----ArgLysThrValThr 613  
 ||||| :  
 Db 4180 GATGTCCTCGGCCAGTAGAGATAATCTGCAATTCTCCAGCAAAGTCAGATAATA 4239  
 Qy 614 GlyLeuAlaGlyAspArgThrLysAspPheHisPheGlu----- 626  
 ||||| :  
 Db 4240 GTCAAAAGGGTGGCAAGGACAATTTCACCGAGATAAGAATGCTCCATTGCGCA 4299  
 Qy 627 -----IleGluLeuLysAsnAsnLys 633  
 ||||| :  
 Db 4300 TCACCTAGCTTGATGAATGAAATTCAATTATGCCCTGAAATAGAGGTCTG 4359  
 Qy 634 GluGluLeuLeuSerGlyThrValLysAspPheAsnLeuGluPhe---LYSAsp 652  
 ||||| :  
 Db 4360 CTGAATTCTTATTAACAACTCAGCAGTATGTTACCCATTGCGGAGAT 4419  
 Qy 653 GLYLYS-----AlaThrIleLeuAsnLeuLysIleGly 662  
 ||||| : : : : : : :  
 Db 4420 GCCGGCAAACCTGGTTATGAAAGTTTCAGTATCCGTACCTCAAGGTAAAGTCAGAT 4479

Qy 663 GluSerLeuThrLeuGlyLysLeuProGluGlyTyrSerTyrLeuValLysGluThrAsp 682  
 :  
 Db 4480 AATGCCCTGACCCCTGACCATATGAAATGGTGCACATATG-----CAA 4527  
 Qy 683 SerGluLysTyrLysValLysAlaAsnSer-----GluValAlaAsnAla 698  
 :  
 Db 4528 TGGCAATCTCTGATCCGCTGAACTCTATTCATTCGGCAGTGTGTTGACCGCC 4587  
 Qy 699 ThrValSerLysThrGlyIleThrSerAspGluThrLeuAlaPheGluAsnAsnLysGlu 718  
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 Db 4588 ACC-----ACCSAAATGATCAATTCTGAGPATGGAAACTCAGATATTAGGAA 4638  
 Qy 719 ProValValProThrGlyValAspGlyLysIleAsnLeuLeuValile 738  
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 Db 4639 CGG-----CAGTGGCAAGGTCTACGTTCTACGTTCTGATA 4677  
 Qy 739 AlaGlyIleSerIleGlyIleTrpGly 747  
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 Db 4678 CCTCCCTATAACCTATCACTCATGGT 4704

RESULT 10  
 US-08-851-567B-46  
 ; Sequence 46, Application US/08851567B  
 ; Patent No. 6528484  
 GENERAL INFORMATION:  
 APPLICANT: Ensign, Jerald C  
 APPLICANT: Bowen, David J  
 APPLICANT: Petell, James  
 APPLICANT: Fatig, Raymond  
 APPLICANT: Schoonover, Sue  
 APPLICANT: french, Constant, Richard  
 APPLICANT: Rocheleau, Thomas A.  
 APPLICANT: Blackburn, Michael B.  
 APPLICANT: Hey, Timothy D.  
 APPLICANT: Merilo, Donald J.  
 APPLICANT: Orr, Gregory L.  
 APPLICANT: Roberts, Jean L.  
 APPLICANT: Strickland, James A.  
 APPLICANT: Guo, Lining  
 APPLICANT: Ciche, Todd A.  
 APPLICANT: Sukhapinda, Kitisri  
 TITLE OF INVENTION: Insecticidal Protein Toxins From Photorhabdus  
 NUMBER OF SEQUENCES: 88  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Dow AgroSciences Patent Department  
 STREET: 9330 Zionsville Road  
 CITY: Indianapolis  
 STATE: IN  
 COUNTRY: US  
 ZIP: 46268  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC DOS/MS-DOS  
 SOFTWARE: Parentin Release #1.0, Version #1.30  
 APPLICATION NUMBER: US 08/395, 567B  
 FILING DATE: 05-MAY-1997  
 CLASSIFICATION: 514  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 08/063, 615  
 FILING DATE: 18-MAY-1993  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 08/851, 567B  
 FILING DATE: 05-MAY-1997  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US 08/608, 423  
 FILING DATE: 28-FEB-1996  
 PRIORITY APPLICATION DATA:



4324 AACGTTCTTACCAACCAAATGCCCATGGTAGATTAGTCACACTCTG 4383  
 QY ||::||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:  
 Db 4384 AATAAACCGGATGATCTTAAGAATATCTTATGACTGAGTAGTAAAGGACTGCFACT 4443  
 QY 601 -----ProValThrHisAsnLeuThrLeu-----ArgLysThrValLeu--- 600  
 Db 4444 GATGTCCTAGGCCAGTAGAGATAATCTGAAATTCTCCAGCAAGTCAGATRATA 4503  
 QY 614 GlyLeuIleAlaGlyAspArgThrLysAspPheHisPheGlu----- 626  
 Db 4504 GTCAAAGGGGTCGCAAGGAGCAACATTACCGCAGATAAGATGCTCCATTACCCA 4563  
 QY 627 -----IleGluLeuLysAsnAsnLys 633  
 Db 4564 TCACCTAGCTTGATGAATGAATTATCAATTAAATGCCCTGAAATAGATGCTCCATTACCCA 4623  
 QY 634 GlnGluLeuLeuSerGlnThrValLysThrAsnLeuGluPhe---LysASP 652  
 Db 4624 CTGAATTATTAACAACTCACGCCAGTTACGTTACGGCTRACTTACCGCATTCGGGAGGT 4683  
 QY 653 GlyLys-----AlaThrIleAsnLeuLysHisGly 662  
 Db 4684 GGCAGCAGACTGGGTATGAAAGTTCTGATATTCTCTTACCCCTCAGGTAAGTACCGAT 4743  
 QY 663 GluSerLeuThrLeuGlyLeuProGluGlyTySerThrLeuLysGluThrAsp 682  
 Db 4744 AATGCCCTGACCCCTGACACATATGAAATGAAATGTCGCAATATPATG-----CAA 4791  
 QY 683 SerGluGlyTyLysValAsnSer-----GlnGluValAlaAsnAla 698  
 Db 4792 TGGCAATCTATGAGTACCTGAACTCATCTGTTGCCGCCAGTGTTGCGACGCC 4851  
 QY 699 ThrValSerLysThrGlyLysLeuAspGluLysLeuAlaPheGluAsnAsnLysGlu 718  
 Db 4852 ACC-----ACCGGATCATACTCTGAGTGGAACTCAGAAATTTCAGAA 4902  
 QY 719 ProValValProThrGlyIvaLysGlyLeuAsnLeuLeuValle 738  
 Db 4903 CCG-----CAGTTAGCCAAAGGTCTATGCTACGGTTGCGATA 4941  
 QY 739 AlaGlyIleSerLeuGlyIleTrpGly 747  
 Db 4942 CCTCCCTATAACCTATCACTCATGGT 4968

---

RESULT 11  
 Sequence 1, Application US/08714402-1  
 Patent No. 5910441  
 GENERAL INFORMATION:  
 APPLICANT: ROCHA, Claudia  
 APPLICANT: FISCHETTI, Vincent A.  
 TITLE OF INVENTION: FIBRONECTIN AND FIBRINOGEN BINDING PROTEIN FROM GROUP A STREPTOCOCCI  
 NUMBER OF SEQUENCES: 2  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
 STREET: P.O. Box 1404  
 CITY: Alexandria  
 STATE: Virginia  
 COUNTRY: United States  
 ZIP: 22313-1404  
 COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/714,402  
 FILING DATE: 16-SEP-1996  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:

NAME: McCowan, Malcolm K.  
 REGISTRATION NUMBER: 39,300  
 REFERENCE/DOCKET NUMBER: 016921-097  
 TELECOMMUNICATION INFORMATION:  
 TELEFAX: (703) 836-2021  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 3531 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)

US-08-714-402-1  
 Alignment Scores:  
 pred. No.: 1.87E-05 Length: 3531  
 Score: 150.00 Matches: 192  
 Percent Similarity: 33.47% Conservative: 127  
 Best Local Similarity: 20.15% Mismatches: 329  
 Query Match: 3.80% Indels: 306  
 DB: 2 Gaps: 50

US-09-494-297-2 (1-757) x US-08-714-402-1 (1-3531)  
 QY 21 LysAsnSerLysArgPheThrValThrLeuVal-----GlyValPheLeuMetIle--- 37  
 ||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:  
 Db 529 AAACCCAGCGGACTTGGACAGTCAGCTTGTAGAGAACGGCTTACCAAGTGTGTTGAA 588  
 QY 38 -----PheAlaLeuThrProAsnAlaLeuAsnProAspSerSerGlyLeuVal 54  
 Db 589 AATCCCTATAATGGGAATCATCAGTAAGCAGGTCAAAGATGTT----- 636  
 QY 55 GluSerSerThrProAsnAlaLeuAsnProAspSerSerGlyLeuVal 54  
 Db 637 ---AGTACTCTTACAGTTGAAATTCCAAATGCACTGTTCTTAATATGGAA 693  
 QY 73 -----TyrGlyTyrglueSerTyvalArgLysHisProTyrtTyrylysInPhe 88  
 Db 694 ACAGAGGTAGTAGTGGCGCAGCGGATVTCACCGAACCACTGCGCTATTTAAATG 753  
 QY 89 Arg-ValAlaHisAspLeuArgValAsnLeuGluGlySerArgSerTyrgInVal-Tyrcy 108  
 Db 754 TCTTTGAGTTGAAACAAGGATAAACCTGAAACAACTCAACCCAGTGATCTTG 813  
 QY 108 SPheAsn-----LeuLys-----LysAlaph 115  
 Db 814 TTAACGGGATGAGCCTCAATCPAAGSTACAGTCAAGATACCCCTPAACATT 873  
 QY 115 EproLeuGlySerAspSer-----SerValLysAspSerPheLysLysHisAspGlyIle 133  
 Db 874 TAGCACAGTGCATAATGCTCCCTGCGATGGAAATAACCTGCTGAGAACCAACT 932  
 QY 133 eserThrLysPheGluAspTVAla----- 141  
 Db 933 TAATCTATACTTCACAGATTATATGCGGTTAGATAAAGTCAGTTGCTGAGAATT 992  
 QY 142 -----MetSerPr 144  
 Db 993 GAGCTTAACTCCCTAGAGATAAGGAAGTTGAAATACTAGTATCTCAAAATTAGAG 1052  
 QY 144 oArgIleThrGlyAspGluLeuAsnGlnLys----LeuArgAlaValMetTyryAsnGl 162  
 Db 1053 TACCATAGTGGCCAGGAGATCACCTAAGGACCGTTAATGTCCTTATGGAAATGAA 1112  
 QY 162 yHsProGlnAsnAlaAsnGlyIleMetGluGlyLeu-----G1 175  
 Db 1113 GAGCCACTAAAGAAAGCATTATTAATCTAATGAGCATGTCGCTGGGAGTTGAA 1172  
 QY 175 uproleuAsnAlaIleArgValThrgInGluAlaValTrpTytySerAspAsnAlaPr 195  
 Db 1173 AACGTAAACAC-----GAACGGGAAATTGCTGTTATGTCACAACTCAA 1226

QY 195 oileserAsn---ProaspGluSerPheLys-----ArgIleuse 207  
   :::||| ::|||  
 Db 1227 CGTRACCAATATTCCTTATGGCAGCATGATTATGGGATTGGAGGGCTCGTCACA 1286  
 QY 207 rgluserAsnLeuValSerThrSerGlnLeuSerLeuMetArgInAlaLeuLysGlnLe 227  
   ::||| ::||| ::|||  
 Db 1287 TACAAGCGACTTAGAACGAGCTAATCAAGTAGTAGTGCTGAGCAGAGAGTCAGGT 1346  
   ::||| ::|||  
 QY 227 uileaspproAsnLeuValSerThrSerGlnLeuSerLeuMetArgInAlaLeuLysGlnLe 227  
   ::||| ::||| ::|||  
 Db 1347 CTATGAAGTACCTGAGGAAGAAATTACCATCACAGTTATGGGTTGAGTCAAACT 1406  
   ::||| ::|||  
 QY 244 -----PhenylSerIlePheGln 250  
   ::||| ::|||  
 Db 1407 TACTTAAGACGGATAACAGCAGGCTAGGAATGGTTCAATACAAACGTC 1466  
   ::||| ::|||  
 QY 250 userGluAspLysGlyAspLys---TyrAspLysGlyTrp 243  
   ::||| ::|||  
 Db 1467 GCGAATTGACTTTGGAATATATCCAAAATAAACGATTTATCATCAAGTAACAGGA 1526  
   ::||| ::|||  
 QY 263 -----GlnAsnLeuLeuSer 267  
   ::||| ::|||  
 Db 1527 AACAGACCACATCTGTAACGCCATGGTTCATCCATTGGCAAGTTTCGTCGGIC 1586  
   ::||| ::|||  
 QY 268 -----S3YGLY----- 269  
   ::||| ::|||  
 Db 1587 TTCTGAATATGCTGCTTFACTCCAGTGAGGAAATGCTACTTCCAAACGAATTC 1646  
   ::||| ::|||  
 QY 270 -LeuValProThrLysProProThr-ProGlyAspProProMetProProAsnGlnProGln 289  
   ::||| ::|||  
 Db 1647 CTTGCTCTCCTCTAAAGGTAGTGGTCTGGAAAGTGAATT----ACTAACGCCCT 1700  
   ::||| ::|||  
 QY 289 nThrThrSerValLeuIleArgLysTyrAlaIleGlyAspTyrSerLysLeu 306  
   ::||| ::|||  
 Db 1701 TATTAACAGTAGCAAATCTAACACAGTGGCTACGTTCCCTTAAGAAATGTCAACTGA 1760  
   ::||| ::|||  
 QY 307 -----LeuGluGlyValThrLeuGluInLeuThrHrgIyAspSerValAsnSerPheGln 323  
   ::||| ::|||  
 Db 1761 CAATGCGCATGGCAGAGCCGCCTTGAGCIGGTTATCAATGGTATAGT---CA 1817  
   ::||| ::|||  
 QY 323 nAlaArgValPheSerSerAsnAspLysGlyLys-----ArgIleGluLeuSerAspGln 341  
   ::||| ::|||  
 Db 1818 GAAATTAGAACGCCAGTCAACACACAAGGAGAGTTCACTTAAAGACTGACCTCGGG 1877  
   ::||| ::|||  
 QY 341 YThrTyrrnLeuThrHrgIleLeuAsnSerProAlaGlyTrpSer 355  
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 Db 1878 CACATATGACCTGTTATGACAACAAAGCGCCAANGGTTTCAGCAGGTCACAGAAANT 1937  
   ::||| ::|||  
 QY 356 -----IleAlaGluProLeuThrPhe 362  
   ::||| ::|||  
 Db 1938 GGCACCGTACTGTGATCAACACTGCTGAGGAAATGGTCACTGGGAAGCCC 1997  
   ::||| ::|||  
 QY 363 -----IysValGluAlaIgLyIysValTyrrnLeuIleAspGlyLysGln 377  
   ::||| ::|||  
 Db 1998 ACATTTGCTCTGAAAGTAGAACGTCACGATGTCACACATAAAAGAAC 2057  
   ::||| ::|||  
 QY 378 -IleGluAsnProAsnLysGluIleLeuValGluProTyrrnLeuValAsnAspHn 397  
   ::||| ::|||  
 Db 2058 CCTTACAGTTTCAGGAAAGAAATTGGCAAG 2096  
   ::||| ::|||  
 QY 397 eGluGluPheSerValLeuThrHrgIlnsTyrrnLeuValGluProTyrrnLeuValAsnAspHn 417  
   ::||| ::|||  
 Db 2097 ACCAGAT-----CAAGCCCCAGCAAGATTCAGTCACACTGTGCA 2138  
   ::||| ::|||  
 QY 417 sAsnGluSerSerGlnValValTyrrnCysPheAsnAlaAspLeuLysSerProAspSe 437  
   ::||| ::|||  
 Db 2139 AATGGTCGA-----AAGATGCTTACCAACGAT 2165  
   ::||| ::|||  
 QY 437 rGluAspGlyGlyLysThrMetThrProaspPheThrThrGlyGluValLysTyrrnThrHri 457  
   ::||| ::|||  
 Db 2166 TCAAGAA-----GTAACGAAAGCT 2201  
   ::||| ::|||  
 QY 457 sIleAlaGlyIyArgAspLeuPheLysTyrrnValLysProargAspHnAspProAspHn 477

---

Db 2202 CTTC-----AAAGCTTGCTTAAGTAGTCAGTGCCAGAAATCAGGG----- 2241  
   ::||| ::|||  
 QY 477 rPheLeuLysHistidineLysValIleGluLysGlyLysArgLysGlyGlnAlaI 497  
   ::||| ::|||  
 Db 2242 -----TAAAGTACTCAGTTGAGAAGTAATGTTCCAGACGGCTACAAAGT 2288  
   ::||| ::|||  
 QY 497 eGluLysSerGlyIleLeuThrGluThrGlnLeuArgAlaAlaThrGlnLeuAlaIleTyrTy 517  
   ::||| ::|||  
 Db 2289 GTCGATTAGGAATAGATATTTAACCCAGA---GAACAGAATHTGTTGTTGACA 2345  
   ::||| ::|||  
 QY 517 rPheThrAspSerAlaGluLeuAspLysAspLysIleLysAspPheTyrrnHisGlyPheGlnAs 537  
   ::||| ::|||  
 Db 2346 GAATRACTTAACCTGAAATTGGAATGCTGAAATAAGGTCATCTGGTCAAAT 2405  
   ::||| ::|||  
 QY 537 pMetAsnAspSerThrLeuAlaValAlaIleLeuValGluTyrrnAlaGlnAspSer 556  
   ::||| ::|||  
 Db 2406 CATTGATGAGACAGCCTAACGCTAACGTTCAAGGAAATTTGGAAAAATGATACGCG 2465  
   ::||| ::|||  
 QY 570 nAsnAsnLysTyryGlnSerIleLeuIleGlyLysIleLeuValGluTyrrnAlaGlnAspSer 585  
   ::||| ::|||  
 Db 2526 TCAACACAAATTATTCGCGTCAGGTAATGAGTCATTGAGTTAAACTTGAA 2585  
   ::||| ::|||  
 QY 586 -----AspLeuVal----- 588  
   ::||| ::|||  
 Db 2586 GAAGTATAATGGAACAGGAATGACATCACTTAAAGACTGACCTCG 2645  
   ::||| ::|||  
 QY 589 -----AspIleIleArgMetGluAspLysGlu 599  
   ::||| ::|||  
 Db 2646 AGGTATGATGTTGACTTACTCAGCTAATGATATTATT-----AAATCCAAACGTTGAGGT 2699  
   ::||| ::|||  
 QY 599 Ile----- 612  
   ::||| ::|||  
 Db 2700 TATTCACACACAAGGACCGAACTAGAGATGAAAGAACGCTTCGGCTAGAATCAGGRC 2759  
   ::||| ::|||  
 QY 612 IThrGlyIleAlaGlyAspArgTyrrnLysAspPheHisPheGluIleGlu 628  
   ::||| ::|||  
 Db 2760 TTCAAGC-----GTAACACTACTGTCGAAAGACTCACGCCACTGTAACCTTACAGG 2813  
   ::||| ::|||  
 QY 647 nLeuGluPheLys-----AspGlyLys-----AlaThrIleAsnLe 659  
   ::||| ::|||  
 Db 2874 TATTAATTCACAAACGCTATTCAGCCAAANGATTGAGTACAGTGAAGATT 2933  
   ::||| ::|||  
 QY 659 uLYRHisGlyIyGluUserLeuThrIleGlu----- 669  
   ::||| ::|||  
 Db 2934 GCGTGATTACTGTTAAACTATVAGTAGCATGGATTAGATGGACAGTGAAGATT 2993  
   ::||| ::|||  
 QY 670 -----LeuProGluGlyTyrrnSerTyrrnLeuValLysGluThrAspSerGluGlyTyrrn 687  
   ::||| ::|||  
 Db 2994 CTACCTGATGCCAGGAAATATAGTT---GRCGAACCGCAGACCGGTATGAA 3050  
   ::||| ::|||  
 QY 687 sVal-----LysValAsnSerGlnGluValAlaAsnAlaIleThrValSe 701  
   ::||| ::|||  
 Db 3051 GATGACAATGCTATACCTTACAGTTATGAGCA-----GGTCAGGTACTGTAA 3104  
   ::||| ::|||  
 QY 701 rLysThrGlyIleLeuThrSerAspGluIleLeuAlaPheGluAsnAsnLysGluProValVa 721  
   ::||| ::|||  
 Db 3105 TGGCAAGGACTAAAGGTCACACTCATATGTCAGGTGATGCTTACAAAGCCACTAA 3164  
   ::||| ::|||  
 QY 721 1ProThrGly-----ValAspIle 729  
   ::||| ::|||  
 Db 3165 GGTTTCAGGTCAGGTTATGATATGAGAAACGCT 3201  
   ::||| ::|||  
 RESULT 12  
 US-09-327-536-1

Sequence 1, Application US/09327536  
; Patent No. 655477  
; GENERAL INFORMATION:  
; APPLICANT: FISCHETTI, Vincent A.  
; TITLE OF INVENTION: STREPTOCOCCIN AND FIBRINOGEN BINDING PROTEIN FROM GROUP A  
; FILE REFERENCE: 022927-008  
; CURRENT APPLICATION NUMBER: US/09/327, 536  
; CURRENT FILING DATE: 1999-06-08  
; PRIORITY APPLICATION NUMBER: US 08/714,402  
; PRIOR FILING DATE: 1996-09-16  
; NUMBER OF SEQ ID NOS: 2  
; SEQ ID NO 1  
; LENGTH: 3698  
; TYPE: DNA  
; ORGANISM: SFBP gene  
; FEATURE: CDS  
; LOCATION: (196)..(3681)  
; US-09-327-536-1

Alignment Scores:  
Pred. No.: 2.02e-05  
Score: 150.00  
Percent Similarity: 33.47%  
Best Local Similarity: 20.15%  
Query Match: 3.80%  
DB: 4  
Gaps: 50  
Length: 3698  
Matches: 192  
Conservative: 127  
MisMatches: 329  
Indels: 306  
QY 21 LYSAsnSerLysArgPheThrValThrLeuVal----GlyValPheLeuMetIle--- 37  
Db 529 AAACCGCCGCACTGGACAGTGTATGAGAACGCGCTATACAACTGGCTGA 588  
Qy 38 -----PheAlaLeuValThrSerMetValGlyAlaValLeuThrValPhedLeuVal 54  
Db 589 AACCCCTATAATGGGAATCATCAGTAAGCAGGGTCAAANGATGT----- 636  
Qy 55 GluSerSerThrProLysAlaAspProSpSerSerSerGluLysArgPr----- 72  
Db 637 ---AGTAGTTCTTACAGTTGGAAAATCCCAAATGTCAGITGTTCTAAATGGAA 693  
Qy 73 -----TyrgLtyrGluSerTyrylValArgLysProTyryLysGlnPhe 88  
Db 694 ACAGAGSGTTAGTAGTGCGCACGGGATTCTACCGAACGCGCTACTTAAATG 753  
Qy 89 Arg-Val-AlaHisAspLeuArgValAsnLeuGluGlySerArgSerTyryGlnValTyry 108  
Db 754 TCTTTGAGTGTGAAACAAAGGAAATCTGAAACAATCAACCACGGTGATACCTTG 813  
Qy 108 SPheAsn-----LeuLys-----LysAlaPh 115  
Db 814 TTACAGCTGGATAGACCTCTCAATCCAAAGGTATCAGTCAGATATCCCTAAATCAT 873  
Qy 115 eProLeuGlySerAspSer-----SerValLysLysTrpLysLysHisAspGly 133  
Db 874 TAGCAc-AGTcAAATGAGTCGCGCTGGATGGAAATACATGCGAGAACCATCAACT 932  
Qy 142 -----MetSerPr 144  
Qy 133 eSerThrLysPheGluAspTyryAla----- 141  
Db 933 TATCTACTTTCACAGATATAATGCGGGTTAGATAAAGTCCAGTTGTCAGAAATT 992  
Qy 144 OarginLeuGlyAspGluLeuAsnGlnLys-----LeuIargAlaValMetTyryGln 162  
Db 1053 TACCATAGGTGGCAGGAGACCATTAAGGAACGGTTATGTCCTTTGGAATGA 1112  
Qy 162 YHISProGlnAsnAlaAsnGlyIleMetGluGlyLeu-----G1 175  
Db 1113 GACCACTAAAGAAAGCATTATATTAATGAGCAATGGGGAGGATTTGA 1172  
Qy 175 uproleAsnAlaIleArgValThrGlyLysGluValIleGluLysValTrpTyrySerAspAsnAlaPr 195  
Db 1173 AAGCTACACACCC----GAACGGGAAATTGCTGTTGATGTCATACTCCAA 1226  
Qy 195 oIleSerAsn---ProAspGluSerPheLys-----ArgGluse 207  
Db 1227 CGGTACCAATATCTCTPATGCCACCATGAATTATGGGATTTGAGGGCTCGTCACAA 1286  
Qy 207 rGluSerAsnLeuValSerThrSerGlnLeuSerLeuMetArgGlnAlaLeuLysGlnLe 227  
Db 1287 TACAGGGACTTAAAGAACGAGCCTAATACAGTGTGCTGAGAGATTCAGGT 1346  
Qy 227 uIleAspProAsnLeuValAlaThrLysSmPrLysGlnValProAspAsp----- 243  
Db 1347 CTATGAACTTCTGAAGGAAATAATCCATCAAGTATGGGATTTGAGGGCTCGTCACAA 1406  
Db 244 -----PheGlnLeuSerIlePheG1 250  
Qy 263 -----GlnAspIleLeuSer----- 267  
Db 1527 AACAGACCAATCTGTAAGCCATTGGCTCAATCCAATTGGCAAGTTTGCCTGC 1586  
Qy 268 -----GlyGly 269  
Db 1587 TCTGAAATATGCTGCTTTACTCCAGTTGGAGGAATGTCCTACTTCCAAAACGAAATTG 1646  
Qy 270 -LeuValProThrLysProProThrProGlyLysProProMetProProAsnGlnProG1 289  
Db 1647 CTGTCCTCTTCAAGGTAGGGTAGGGTCTGGGAAAGGAAATT-----ACTAACGCTC 1700  
Qy 289 nThrSerValLeuIleArgLysTyraAlaIleGlyLysAspTyrySerLysLeu----- 306  
Db 1701 TATTACAGTGGAAATCTAAACGAGTGGCTCAGCTGCTGCTTAAGAAAATGTCACGTGA 1760  
Qy 307 -----LeuGluGlyIaThrLeuGluLysLeuThrGlyLysAspValAsnSerPheG1 323  
Db 1761 CAATGTCCTCATGGCCAGAACGGCTTGTGAGCCTGGTTCATCAATGTTAATGTT-----CA 1817  
Qy 323 nalaArgValPheSerSerAspAspIleGlyLys-----ArgIleGluLeuSerAspG1 341  
Db 1818 GAAATTAGAAGCCGATTCACACACAGGAGGGTCACTTTAAGGACCTGACCCGG 1877  
Qy 341 YHITTYrThrLeuThrGluLeuAsnSerProAlaGlyTyrySer----- 355  
Db 1878 CACATATGACCTGTGATGAAACAGGCCAAAGGTTACGCGGTGACAGAGAAATT 1937  
Qy 356 -----IleAlaGluProLeuIlePhe----- 362  
Db 1938 GGCGACCGTTACTGTGATCACTTACCAAAACCTGCTGAGGAATGTCCTACTGGGAAGCCC 1997  
Qy 363 -----LysValGluAlaGlyLysValTyryThrIleIleAspGlyLysGln----- 377  
Db 1998 ACATTCGCTCTGAAATGAGCTAACAAAGAACGTCAGATGTCACCATAAAGAAAC 2057  
Qy 378 -IleGluAsnProAsnTyryGluIleValGluProTyrySerValGluIleValAspAsp 397  
Db 2058 CCTTACGTTTCAGGGAGAAATTGGGAG-----ATGACAG 2096  
Qy 397 eGluGluPheSerValLeuThrGlnAsnTyryAlaLysPheTyryTyryAlaLysAsn 417  
Db 2097 ACCAGAT-----CAACGCCAGCAAGAATCAAGTCACGTGCACTGTGCA 2138  
Qy 417 SASnGlySerSerGlnValTyryCysPheAsnAlaAspLeuLysSerProProAspSe 437



Oy	99 GluGlySerArgSerTyrGlnValtyrCysPheAsnLeuLys-----	112
Db	1735 CAAGCTATGGGTCATAATACTGTTCAATTAACTACAAACAAAATTAGGAATGAA 1794	Db
Oy	113 ----LysAlaPheProLeuGlySerAspSerSerValLysLysPheAsnAlaAspLeu	414 ----AlaLysAsnLysAsnGlySerSerSerSerSerValValValtyrCysPheAsnAlaAspLeu
Db	1795 CAGCAAAAGAGCTTGTTAATAATTCAAGCT-----TGCTATCAGAGCT 1842	Db
Oy	131 AspGlyIleSerThrLysPheGluAspPyrrAlaMetSerProArgIleThrGlyAspGlu 150	Qy 432 LysSerProProAspSerGluAspGlyLysLysThrProAspPheThrThrGly 451
Db	1843 GGT-----AGGAAGAAGTGACGGAAATCA 1869	Db 2746 GTAAAGACTCACACAGACATCACGGTACGACATACAGATACACAGGA 2805
Oy	151 LeuAsnGlnLysLeuArgAlaValMetIrrAsnGlyHisProGlnAsnAlaasnGlyLe 170	Qy 452 GluValLysTrpThrHistIleAlaGlyArgAsp-----
Db	1870 TTTAACATCATACTGTC-----ACAATATTAACTGCTTAATGCCGGT 1908	Db 2806 GAGACATCGGCAACAGTAGAACAAATGGCATGACAATAATACCAAGAGGAAACGA 2865
Oy	171 MetGluGly-----LeuGluProLeuAsnAlaLeuArgValThrGlnGlu 185	Qy 463 -Leuhe-----LysTrpThrValLysProArgAsp 472
Db	1909 ATTGAGGTTACTGTAAGGGAATTAAGTTAAACAGGATAAGATCCAG----- 1965	Db 2866 CCAACTGAAATCAAAGTTGAGTTATCAAGACGCAAACAGGAAACA 2925
Oy	186 AlaValIrrPTyTySerAspAsnAlaProIleSerAsnProAspGluSerPheLys--- 204	Qy 473 ThraspProAspThrPheLeuLysHissileLysValIleGluLysGlyTyrrGlu 492
Db	1966 -----GCTCTATAGCTATT 1995	Db 2926 TTAATGAACTTAATACTGGACCCATAGTGGACAGGATTAGTCAA-----AAAGCA 2979
Oy	205 ArgGluSerGluSerAsnLeuValSerThrSerGlnIleSerLeuMetArgGlnAlaLeu 224	Qy 493 LysGlyGlnIlaIleGluLysSerGlyLeuThrGluLysValIleGluLysGlyTyrrGlu 512
Db	1996 TCTAAAAAGATGATGAGTCACTGTTAAAGCACAATCAA-----AAAGAAATT 2040	Db 2980 AAAGGACAACAGTAATACAGTCGAGGAAATTACAGTCGAGGATTACAA 3039
Oy	225 LysGlnIleUleAspProAsnIleUalAthrlsMetProLysProGlnValProAspPhe 244	Qy 513 -LeuAlaIleTrpThrPheThrAspSer 521
Qy	2041 GAGATATAACAGATGAAACGGTATGCTAATAATTAAGCGTGCCTAGTGGAGCATT 2100	Db 3040 CATGTCGATACAACTGATATGGGTAACTTGATGTCGACGAAATAATACCCGAGAAC 3099
Db	2161 TTTACTATGAAAGATACAGATATCAGGGATATTGACTATTTGAAATGCAAAGCG 2220	Qy 522 AlaGluLeuAspLysAspLysLeuLysAspPyrrHisGlyPheGlyAspMetAsnAspSer 541
Oy	245 GinLeuSerIlePheGluSerGlu-----AspLysGlyAspLysTrpYr--- 258	Db 3100 ACATCAATTAGTGGTCAAAAGATATGGAC 3141
Db	2101 ATTTTAAAGAAATAGAGGCCACGACGGTATACTATTGATAGGATAAAGATATCG 2160	Qy 542 ThrLeuAlaValAlaLysIleLeuValGlyIlaGlnAspSerAsnProGlnLeu 561
Oy	259 -----AsnLysGlyTrgIlnAsnLeutSerGlyIleu--- 270	Db 3142 -CAAGTGGTAAGAGCAGAAAA 3165
Db	2161 TTTACTATGAAAGATACAGATATCAGGGATATTGACTATTTGAAATGCAAAGCG 2220	Qy 562 ThraspleuAspPhePheIleProAsnAsnLysTrpCinSeLeu-----Ile 578
Oy	271 -----ValProThrLysProProThrProGlyAspProProMetPro 284	Db 3166 GTCACTGTTGAT-----TTATRGCTGATGGAGAGAAGTAGAAAACGTTAGAGCTGACATCT 3222
Db	2221 ATAGAAAAACAAAGATGTTCTGCTCAAAGGTTGGAAAGGCACTCAAAGTGAA 2280	Qy 579 GlyThrGlnTrpHisProGluIleAspLeuValAspIleLeuGmetGluAspLysLysGlu 598
Oy	285 ProAspGlnProGlnThrThrSerValIleArgLysTrpIlaIleGlyAspTyrSer 304	Db 3223 GAACAACTGGAAGTACGAA-----TTAACGACTTACCGAGATATGGAC 3279
Db	2281 CCA-----ACGATTATTCAGTGTACACAAAGATGACATCA 2322	Qy 599 ValIleProValThrHisAslLeuThrArgLysThrValThrGlyLeuAlaGlyAsp 618
Oy	305 -----LysLeuLeuGluGlyAlaThrLeuGlnLeu 314	Db 3280 ATA-----GAATATACAGTGACC-----GAAGAT 3303
Db	2323 AATACAAACACCACTAGACAACAGAGATTAAGAAATGAGATGGACGAAAAAGTG 2382	Qy 619 ArgThrLysAspPheHisPheGluLe-----
Oy	315 ThrGlyAspAsnValAsnSerPheGlnAlaArgValPheSerSerAsnAsp---IleGly 333	Db 3304 CACGTTAAAGACTACACAAGACATCAAGGTTAGGACAAATACGACATACACCA 3363
Db	2383 ACATGTCCTAACTT-----CCGGAAATGACAACAAATGCC 2418	Qy 628 -----GlutLeuLysAsnAsnLysGlnGluLeu 636
Oy	334 GluArgIleGluLeuSerAspGlyIleThrIrrLeuThrGluLeuAsn----- 349	Db 3364 GGAGAGACATGGCACACGATACACAAACAAATGGATGACAAATAATACGACGGAAA 3423
Db	2419 AACGCTTAATAA-----TATGGCTCAAGTGAA 2463	Qy 637 LeuSerGlnThrValLysIleAspLysThrAspLysIleLeuGluPheAspGlyLys----- 654
Oy	350 -----SerProAlaGlyTyrsSerIleLeuGlu----- 358	Db 3424 CGACCAACTGAAATCAAGTGTGATTA-----TATCAAGACGGAAACAA 3471
Db	2464 GATACAAACACCAAGAAGTATACATAAAAGAAATGGTTAGTGTACTAACTGAA 2523	Qy 655 -----AlaThrIleAsnLeuLysHisGlyGluSerLeuThrIleGlyIleu----- 670
Oy	359 --Prole--ThrPheLysValGluAlaGlyLysValTyrrThrIleLeuAspGlyLys 376	Db 3472 GGAAAACCGCACATTAATGAACTTAATACTGACCCATACCTGGACAGGATAGAT 3531
Db	2524 AAACCAATCGAACACACATCAATGAGTGTGAAAGAGTATGGACGACAACATCA 2583	Qy 671 -----ProGluGlyTyrsSerTyrrLeuValLysGlu---ThraspSerGluGly 685
Oy	377 GluIleGluAsnProAsnLysGluIleValGluIleProTyrsSerValGluIlaTyrrAsnAsp 396	Db 3532 GAAAAGCAAAACACACACACTAAATACACAGTCGAGGATTAACAGGTCAAGGT 3591
Db	2584 GATGGTAAAGAGGACGAAAGA-----GTCAGTGTGAAATTGGCTCA 2628	

Qy 686 TyrLysValLysValAsnSerGlnGluValAlaAsnAlaThrValSerLys----- 702  
Db 3592 TATACAAACATGATGATAACATGATGGCAACTTGTGAGCATAATAACG 3651  
Qy 703 -----ThrGlyLleThrSerAspGluThrLeuAlaPheGluAsnAsnLysGluPro 719  
Db 3652 CCAGAACACATCAATTGGTGAAGAATGATGGACGACAAGACATCAGATGGT 3711  
Qy 720 ValValProThrGlyValAspGlnLysIle-----AsnGly 731  
Db 3712 AAGAGACCAGAAAAGTCAGTGTAATTTATGGCTAACCGA 3753  
**RESULT 14**  
US-09-071-035-457  
; Sequence 457, Application US/09071035  
; Patent No. 6448043  
; GENERAL INFORMATION:  
; APPLICANT: GIL H. Choi  
; TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides  
; NUMBER OF SEQUENCES: 496  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: Maryland  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
; COMPUTER: HP Vectra 486/33  
; OPERATING SYSTEM: MSdos version 6.2  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/071,035  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: A. Anders Brookes  
; REGISTRATION NUMBER: 36,373  
; REFERENCE/DOCKET NUMBER: PB369P2  
; TELEPHONE: (301) 309-8504  
; TELEFAX: (301) 309-8512  
; INFORMATION FOR SEQ ID NO: 457:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6168 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; US-09-071-035-457  
Alignment Scores:  
Pred. No.: 5.94e-05  
Score: 149.00  
Percent Similarity: 32.02%  
Best Local Similarity: 19.26%  
Query Match: 3.78%  
DB: 4  
Length: 6168  
Matches: 181  
Conservative: 120  
Mismatches: 320  
Indels: 320  
Gaps: 45  
Db 3481 TTGGCTGGGTGCCACAAGGCCATACATTGGGGAGACAAGCACCA----- 3531  
Qy 63 AsnProAspSerSerSerGlyUrgArgTrpGlyUrgLysSerLys 82  
Db 3532 ----- 3552  
Qy 83 ProTyroTyrylsglPheArgValAlaHisAspLeuArgValAsnLeuGluGlySerArg 102  
Db 3553 GAATTAGCTAAAGCCGAGTCATTCATGAGAAGAACTTCAGCCGAAGGCACAA 3612  
Qy 103 SerTyrGlnValTycysPheAsnIeuLysAlaPheProElySerAspSer 122  
Db 3613 CCA--ACCATTAAACGATGCTAAAGTATTAGAAAMATGGAGAG 3669  
Qy 123 ValLysLysIrp-----TyrylLysIisAspGlyIleSerThrLysPhe-- 137  
Db 3670 GGTAAGAAAGTAGTCATGCTCGCTTAATAGCAGTCAGCCGAAACCACGGTTACT 3729  
Qy 138 -----GluAspTyrlAlaMetSerProArgIleThrGlyAspGluLeuAsnGlnLysIeu 155  
Db 3730 CATGGGAGAAGTCCTCCCGTGGCGGTGCGAACCC 3765  
Qy 156 ArgAlaValMetTyrlAsnGlyHisProGlnAsnAlaAsnGlyIleMetGlu----Gly 173  
Db 3766 -----AAGCGAATGGCCAGTAGGAGGTAGT 3795  
Qy 174 LeuGluPro---LeuAsnAlaIleArgValThrGlnGluValAlaValTrpItyrSerAsp 192  
Db 3796 TTAAKACCAGGCCTTATAGTCAGTCACAGAAATCAGAGCCGACAATTCGTGATGTTCAT 3855  
Qy 193 AsnAlaPro----- 195  
Db 3856 ACGACCCCCAACGATCATCGTGAACACAAATACGAGCGGACAATTCGTGATGTTCAT 3915  
Qy 196 -----IleSerAspProAspGluSerPheLysArgGluSerGluSerIasn 210  
Db 3916 GTCAAAATGCTTAATACCAAGGTTCTGACTTAATAAAAGACCAAGCAGGCCAT 3975  
Qy 211 LeuValSerThrSerGlnLeuSerLeuMet-----ArgGlnAlaLeuLysIeu 226  
Db 3976 CCATTAAGCTGGTGAATTTCAGCCCTGACACACAGGACAGGAGCAGGAGCTTCAGAAC 4035  
Qy 227 --LeuIleAspProAspAsnLeuAlaThrLysMetProLysGlnValProAspAspPheGln 245  
Db 4036 TTAGTTTCGATGCAAACGGAAAGTCACAGTGGAGGATTAGCCCCAGGAAATAACAA 4095  
Qy 246 LeuSerIlePheGluUserGluAspDlyGlyAspLysItrAsnLysGlyTyrglnAsnIeu 265  
Db 4096 TTT-----GTGGAACCAAGGCCA----- 4116  
Qy 266 LeuSerGlyGlyLeuValProThrLysProProThrProGlyAspProPrometProPro 285  
Db 4117 --GCAGGGTACCTTTAACACIGGACCAAGTCCTTCACGTTGCGCAAGCGATCG 4173  
Db 4234 TTAACTAAAAAGATGTGAATGGA-----CAGTTAAGTGGGCGACATTAA 4284  
Qy 286 AsnGlnProGlnThr----- 293  
Db 4174 GGCAACACGCAACGTTATAGCAACGGCTAACCTATCAAGGCAAGCTAA 4233  
Qy 294 LeuIleGlyLysItrAlaIleGlyAspTyrSerLysIleLeuGluGlyIalathrLeuGln 313  
Db 4234 TTAACTAAAAAGATGTGAATGGA-----CAGTTAAGTGGGCGACATTAA 4284  
Qy 314 LeuThrGlyAspAsnValAsnSerPheGlnAlaArgPheSerSerAsnAspIle 333  
Db 4285 GTGCTGATGCGGAGGGAGAACGCTAACACGGCTG--ACGACAAATACTAACGG 4341  
Qy 334 GluArgGly-----GluLeuUserAspGlyIthTyrrLeuIleGluLeuAsnSerPro 351  
Db 4342 GAAATGTTGCGAGGCACTTAGCCGAAATACTCCTTGTAGAAACCAAGCGCCA 4401  
Qy 352 AlaGlyTyrsErle--AlaGluProIleThrPhyLysVal-----GluAlaGly 367  
Qy 19 LeuSerLysAsnSerLysArgPheThrValIleuValGlyValPheLeuMetIlePhe 38  
Db 3361 CTGAGAACACAGGCTGAGGAGACGACTTGTGAGGCCATTCCAAATTG 3420  
Qy 39 AlaLeuValThrSerMetIal-----GlyAlaLysIthr 49  
Db 3421 GACCAAGCTAAACACAAGCTCTACGTGAAGGTACAGTGTAGATGCCACCGGGTTATCACAA 3480  
Qy 50 ValPheGly-----LeuValGluUserSerThrProAsnAlaIle 62

Db 4402 ACAGGGCTTTTAAATACCAAGCCAGTCCCATTGAAATTCTGAGAAAATGCTGGT 4461  
Qy 368 Lys----- ValTyrThrle 372  
Db 4462 AAACCAGGGCTGTGGTTGCTAGTGCACACTTGTGAGTTACAAGGGCTTTCAAATC 4521  
Qy 373 ILEASPGLYLysGlnIleGluasnPro----- 381  
Db 4522 CGAAACAGGAAACCTAGCGGAGACCACTATAGCAGGTCGTTTGAAATAATGATCAC 4581  
Qy 382 AsnLysGluIleValGluIleProtyrSerValGluAlaItyrAspAspPheGluLpheSer 401  
Db 4582 AATAAACA-ATCATAGGATTACAGC-----  
Qy 402 ValLeuThrThrGlnAsnTYR-----  
Db 4626 -----CNAATAATTCTTAGAGACTTGGCCAGTACTTATACAAAGA 4673  
Qy 416 D-----LysAsnGlySerSerGlnValValTyrcys----- 426  
Db 4674 AATCAAAGCACCACAAATTACCAAGATGCCGAGATTATATTATCCTGATTAGTAA 4733  
Qy 427 -----PheAsnAlaAspLeuIysSerProProAspSerGluAspCylGlyLysThrMe 444  
Db 4734 AGTAGAAATTCTGGGATTCAGGATCGGGACATT----- 4773  
Qy 444 tthrProAspPheThrThrGlyluValLysTyrrhHisIleAlaGlyArgAspLeuPh 464  
Db 4774 -----TCCAATTAGGG-----GCCCTTCGCCATTCAAGGACGCCGCCGCTT 4817  
Qy 464 eIystY-ThrValLysProArgAspThrAspProAspThrPheLeuIysHistidylsly 484  
Db 4818 TAAAGAAATTGATGCCATGCCAACCCACTTCCAGGACGATTTAACATGATGCA-- 4875  
Qy 484 svalleGluLysGlyItyrArg-----  
Db 4876 -----ATCCAAACGGGAAATACTTGAAGAGAACTGCTGAAANAGATGTC 4931  
Qy 4956 alle-----  
Db 4932 ATGGCTATGGAGGATTAGGTGCTGCTAGCTATGAAATTAGTAAGCTGGATGCAACGGA 4991  
Qy 506 nieuargaalaalathrglnleuAlaIleTyryrPhe-----  
Db 4992 TGGCTATPATCGTCATAAACACCCATTATTTGATGAGAAAGAATTCAAATGATAA 5051  
Qy 521 ralaGluLeuAspLysAspLeuIysAspTyrrhIsGly-----  
Db 5052 ACAACCACTAGTAGGTTAGCTGAAATTCAACGAGAGTAATGGACGTAAGT 5111  
Qy 537 -AspmetaasnaspSerThrLeuAlaLysIleLeuValGlyItyrAlaGlnAspse 556  
Db 5112 CAACGAGCAAGTCATAACACTTACGGGTGCAATTACATGCCGATGAGCA 5171  
Qy 556 rasnProProGlnIleThrAspLeuAspPhePheIleProasnAsnAsnLysTyrginse 576  
Db 5172 GAATCAGCCCAAGGTACCGATAACATCTCTGAATCGTCGAGGAGAAAGTTCTGA 5231  
Qy 576 r-----  
Db 5232 AATACACACGGATAAGACTGGCAATTACCTAAGGGCTAAATGAGGGCATTAAGT 5291  
Qy 577 -----LeuIleGlyItyrIleLeuIleLeuValGlyItyrAlaGlnAspse 586  
Db 5292 TTAGTGGAAACGAAAGCACCACAGGCTATCTGTRAGACACACGGCTACATCCA--- 5346  
Qy 586 pheuvalAspIleAspIleLeuIleLeuIleLeuValIleProvalThrHisAsnle 606  
Db 5347 ---TTAGTGGAAACGCACTGGCCCAATTAGGAAGAGCAGCCAAATGCTTTAGGGATCTT 5402  
Qy 606 uthrLeuIleGlyIleLeuIleLeuIleLeuIleLeuIleLeuIleLeuIleLeuIle 626  
Db 5403 CAATTATCAAGGAACTGCT-----CA 5423

Qy 626 uileGluLeuIysAsnAsnLysGlnGluLeuIeuserGlnThrVal-----LySthras 644  
Db 5424 ATTACCAAAGAACGAAACAGGTGAAGCATGCGAGTGGGGGTTAAAGTCATG 5483  
Qy 644 pheThrAsnLeuIgLuPhelyAspGlyLysIlaThrle--AsnLeuIsh1S1Gyl 663  
Db 5484 TGAAACAGG---CAAACCGTAGTGGACAAACCAACTGATGTCGACAAAGCAAGC 5540  
Qy 663 uSerLeuThrLeuIglnGlyLeuProGluIgLyTyr----- 674  
Db 551 AGTCATGCGAAAActTAGCACGGGACGTTGAGGAGACACAGGCCAC 5600  
Qy 675 -SerTyryeuvalLysGluThrAspSerGlnValValTyrcys----- 687  
Db 5601 TAGCTATCTCTTAATGAAACGCCAAGGCCAAGCTTACGATGCCAAAGACCAAGG 5660  
Qy 688 -ValLysValAsnSerGlnGlyIleuIalaAsnIla----- 698  
Db 5721 GCGGAAATTGTCAGCAGAACGATGCTTACGAGGCTGAAATTAACTGACAGATC 5780  
Qy 699 -----ThrValSerIsthrGlyIleuIleSerAspGlyIleuIalaIlePheG 714  
Db 5781 AGAGACAGGCCAACCTGRCGCTGTTACAGTCTGACACACCCAGGGTTAGTCAGT 5840  
Qy 714 usnAsnLysGluProValProArgIlyvalAspGlnLysIle--AsnGlyWY 732  
Db 5841 GAACACACTTACAAACGAAATACTTGGGAAACAAAGCACCGGATGTTAC 5898

RESULT 15  
US 09-071-035-461  
: Sequence 461, Application US/09071035  
: Patent No. 6418043

GENERAL INFORMATION:

APPLICANT: Gil H. Choi

TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides

NUMBER OF SEQUENCES: 496

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20850

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MS DOS version 6.2  
SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/071, 035  
FILING DATE: 07/07/2003  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
FILED DATE:

ATTORNEY/AGENT INFORMATION:  
NAME: A. Anders Brookes  
REGISTRATION NUMBER: 36, 373  
REFERENCE/DOCKET NUMBER: PB369P2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (301) 309-8304  
TELEX: (301) 309-8512  
INFORMATION FOR SEQ ID NO: 461:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6168 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear

us-09-071-035-461

Alignment Scores:  
Pred. No.: 5.94e-05  
Score: 149.00  
Percent Similarity: 32.02%  
Best Local Similarity: 19.26%  
Query Match: 3.788  
DB: 4

US-09-494-297-2 (1-757) x US-09-071-035-461 (1-6168)

QY 19 LeuSerLysAsnSerLysArgPheThrValThrLeuIvaGlyValPheLeuMetIlePhe 38  
Db 3361 CTGAAGAACACAGCATTGTGATGAGACGACTTCTTAGCAAGGCCCATTCGAATTG 3420

QY 39 AlaLeuValThrSerMetVal 45

Db 3421 GACCAGCTAAACACAGCTCTACGGTAAGGTACAGTAGATGCACCCGGGTATCAA 3480

QY 50 ValPheGly 49

Db 3481 TTGCGGGTGCACAAGGCAATACATTTGGGGAGCACAAAGCACAA 3531

QY 6 AsnProAspSerSerSerGluTyRArgTPtyRArgTyRGlusSerTyRAlaArgValPheSerSerAsnAspIleGly 82  
Db 3532 -----  
Db 3553 GAATAGCTAAAGGCCAGCTCATCTACTATGATGAGAACTTCAGCCAGGGACACA 3612

QY 8 ProTyRTyRArgGlnPheArgValAlaHisAspLeuArgValAsnLeuGluGlySerArg 102

Db 3613 CCA--ACATTATTAACAGCAGTGCAATAAGATTGTTAGAAAATGGTGAGAAG 3659

QY 123 ValLySlysIlePhe-----TyRArgLySHisAspGlyIleSerThrLySphe--- 137  
Db 3670 GGTAAAGAATGTTAGCAATGCTCGCTTAATAGGCAVCCGTRACCAAGCCGTTACT 3729

QY 138 -----GluAspTyRAlaMetSerProAspIleArgIleArgIleAspGluLeuIspGlnIleIle 155  
Db 3730 CATGGGAGAAGTTCCTTGCGCGGGATGAAAC----- 3765

QY 156 ArgAlaValMetTyRAsnGlyIleProGlnAsnAlaAspGlyIleMetGlu----Gly 173  
Db 3766 -----  
Db 3795 TAAACACGGGCTTATGTTACAGAACGAACTCGAACGCCGACAGCTTCTTAGAC 3855

QY 174 LeuGluPro--LeuAsnAlaIleArgValThrGlnGluAlaValTrpTyRArgSerArg 192  
QY 193 AsnAlaPro 195

Db 3856 ACCACCCCACACGATTCTGGACACAAATAGGAGGAGCACAAATGCTGATGTCAT 3915

QY 196 -----IleSerAsnProAspGluSerPhylsArgGluSerGluSerAsn 210  
Db 3916 GTCAAATGCTTAATTAACAGGTTCTGTTGAACTAATPAAAAGAGCCAAAGGCCAT 3975

QY 211 LeuValSerThrSerGlnIleSerIleMet-----ArgGlnAlaLeuIlePheGln 226

Db 3975 CCATAGCAGGTCTGAAATTGACGCCAACGGACAGCAGTCGAGAACAC 4035

QY 227 ---LeuIleAspProAsnIleAlaThrIleSerMetIlePheGlnValProAspPheGln 245

Db 4036 TTGCTTCGATGCHAACGAAAAGTCACAGTGGAGTTAGCTGCCACAGAAATCA 4095

QY 245 LeuSerIlePheGluSerGluAspLysArgIleAspLysAspTyRArgIleAsnIle 265  
Db 4095 TTT-----GTGCAACAAAGGCCA----- 4116

QY 266 LeuSerGlyGlyLeuValProThrLysProProThrProGlyAspProProMetProPro 285

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Db 4117 ---GCAGGGTACCTTTAACACGAACTGCTTCACGATTGCAACAGGATCGG 4173  
QY 286 AsnGlnProGlnThr----- 293

Db 4174 GGCAAAACCAACAGTATAGCACGCTAACTTGTAACTATCAAGGCAGCTAA 4233

QY 294 LeuIleArgLysTyRAlaIleGlyAspTyRSerLysLeuLeuGluGlyAlaThrLeuGln 313

Db 4234 TTAACTCAAAAGTAGTGTGATGGA-----CAGTTATAAGTGGGCGACATTAA 4284

QY 314 LeuThrGlyAspAsnValAsnSerPheGlnAlaArgValPheSerSerAsnAspIleGly 333

Db 4285 GTGCTTGATGCGAAGGGAGAACGATTCACACGGCTTG-----ACGACAAATACTCAAGGG 4341

QY 334 GluArgIle-----GluLeuSerAspGlyIleThrLeuThrGluLeuAsnSerro 351

Db 4342 GAAATGTTGCGAGCAACTTACGCCAGAACAAATCGCTTGTAGAGAACCAAGGCCA 4401

QY 352 AlaGlyTyRSerIle---AlaGluProLeuThrPheLeuVal-----GluAlaGly 367

Db 4402 ACAGGCTATTATTAATACACGCCAGTCCCATTTGAATATTGCTGAGAAAAATGCTGGT 4461

QY 368 Lys----- 372

Db 4462 AACCCAGCGCTCGTGTGCTAGTCAACACTTGTGAGITACAAAGGGCTTTCACATC 4522

QY 373 IleAspGlyIleGlyIleGluAsnPro----- 381

Db 4522 GTGAAACGATAGGGCAGCCAACCATAGCAGGGCTGTTTGAATTATGATCAC 4581

QY 382 AsnlysGluLeuValGluProTyRSerValGluAlaTyRAsnAspPheGluGluPheSer 401

Db 4582 AATAACA-ATCATTTAGGGATTACGC-----AACGATGGCNAAGATGG-- 4625

QY 402 ValLeuThrThrGlnAsnTyR-----AlaLysPhe-TyRTyRAlaLysAS 416

Db 4626 -----CAAAATTCTTGTAGACTTGGGCCAGGTTACTANTATTACAAANGA 4673

QY 416 n-----LysAsnGlySerSerGlnValValValTyrcs----- 426

Db 4674 AACCAAAGCCAAATTAACAGGTTGGCCAGATATAATTTCTGAAATTGTTAA 4733

QY 427 -----PheAsnAlaAspLeuLysSerProProAspSerGluAspGlyGlyIleIle 444

Db 4734 AGTAACTTCTGGTGATTCAAAGGTGATCCGGAGATT----- 4773

QY 444 tThrProAspPheThrThrGlyIleValLysTyRThrHisIleAlaGlyArgAspLeuH 464

Db 4774 -----TTCCATTAGGG-----GCCTTCGCCAAATTCAAAGGACGCCGCGCT 4817

QY 464 eLysTyRThrValLysProArgAspThrAspProAspThrPheLeuIleHisIleLysLys 484

Db 4818 TAAGAAATTGTGCCAAATCGAACCCACTTCGAGAACGATTTTAAATGTCATGA-- 4875

QY 484 svalIleGluLysGlyTyRArg-----GluLysGlyGlnAl 496

Db 4876 ---ATCGAAACGGGGAAAATCTTGTAAAGAGAACTGCTGAAAAGATGGTC 4931

QY 496 alle----- 506

Db 4932 ATGGCTTATGGAGGATTAGGTGCTGGTAGTGTGAAATTGATGACGCTGACGAA 4991

QY 506 nLeuArgAlaAlaThrGlnIleUalIleIleIleIle 521

Db 4992 TGGCTTATGTGCTGATTAACACCACTTGTGAGAAGAAATTCAAATGATAA 5051

QY 521 IleGluIleAspLysAspLysLeuLysAspTyRHisGly-----PheGly----- 536

Db 5052 ACAACCACTAGATGAGTAGTTGTGAAATTAACTGAGAAAGTAATGGGACGTTAAAGT 5111

QY 537 -AspMetAsnAspSerThrLeuAlaValAlaLysIleLeuValGluIlePheGlnAspSe 556

Search completed: August 19, 2003, 18:23:10  
Job time : 211 secs

